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OM protein - protein search, using sw model

November 8, 2004, 08:05:27; Search time 44.8163 Seconds (without alignments) 3132.595 Million cell updates/sec Run on:

US-09-830-693B-27 1250 1 SLALSLTADQMVSALLDAEP......CKNVVPLYDLLLEMLDAHRL 244 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P03372 homo sapien	Ofgis5 bos taurus		P19785 mus musculu	P06211 rattus norv	Q29040 sus scrofa	Q9qzj5 mesocricetu	Q8uwb0 caiman croc		Q91250 poephila gu	gallus ga	Q765n7 alligator m	Bad08348 alligator		Q8cgk8 cavia porce			Q9yht3 anolis caro	Q6w5g5 xenopus lae	Aaq84784 xenopus l	Q6w5g9 xenopus tro	Aaq84780 xenopus t	Q6w5g7 xenopus lae	Aag84782 xenopus l	P81559 xenopus lae	Q6w5g6 xenopus lae	œ	Q91424 cnemidophor			Q7t2k8 halichoeres
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# ALIGNMENTS

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                                                                            SEQUENCE OF 110-117, PHOSPHORYLATION, AND MUTAGENESIS
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X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 180-262.
MEDLINE=94037103; PubMed=8221895;
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[12]
INTERACTION WITH NCOAS.
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306 SPVLSLTADQMISALLEAEPPIIYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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        SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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96.4%; Score 1205.5; DB 2; Length 596;
Best Local Similarity 95.9%; Pred. No. 1.2e-92;
Matches 235; Conservative 5; Mismatches 4; Indels 1;
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Nishimura N., Tetsuka M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY538775; AAS46251.1; -.
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ID ESRI_MOUSE STANDARD;
AC P19785; Q9JJT5; Q9QY51; Q9QY52;
DT 01-FEB-1991 (Rel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                   FDMLLATSSRFRMMNLQG-EFVCLKSIILLINSGVYTFLSSTLKSLBEKDHIHRVLDKITD 179
                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                     PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNGCKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHNSNKGMEHLYSMKCKNVVPLYDLLLEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCOA6 coactivators, leading to a strong increase of transcription of target genes.
                                                                                                                                                                                               SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                        Gaps
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Mishimura N., Tetsuka M.;

Mishimura N., Tetsuka M.;

Nishimura N., Madaga to the muclear hormone receptor family.

Nishimura N., Madaga to the muclear hormone receptor family.

Nishimura Ni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Euthéria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Bovinae, Bos.
1.1 TaxID=9913,
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                                                                                       595;
                                                                              Query Match
99.2%; Score 1239.5; DB 1; Length
Best Local Similarity 99.6%; Pred. No. 1.7e-95;
Matches 244; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estrogen receptor alpha.
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Matches 235; Conserv
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RC STRAIN=CS7BL/6J; TISSUE=Done, and Thywnus;

RK SEQUENCE FROM N.A.

RADINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA KAZARIY Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka H., Kiyosawa H.,

RA Vagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,

RA Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B.L., Lyons P.A.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B.L., Miki H.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Maglott D.R., Wallais R., Pontius J.U., Qi D., Ramachandran S.,

Perrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Tesadale R.D., Tomita M.,

Kaning L.G., Wynshaw-Boris A., Yanagi Sawa M., Yang I., Yang I.,

Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayateu N.,

Khing L.G., Wanshaw-Boris A., Yanawa W., Arakawa T., Fukuda S.,

Hara A., Hashizume W., Imotani K., Ishii Y., Icho M., Sakazume M.,

Barney E., Hayashizaki Y.,

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Kos M., O'Brien S., Flouriot G., Gannon F.;
Trisue-especific expression of multiple mRNA variants of the mouse
estrogen receptor alpha gene.";
FBSS Lett. 477:15-20(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97153020; PubMed=8999954;
Jiang M.S., Hart G.W.;
"A subpopulation of estrogen receptors are modified by O-linked N-
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 269-599 FROM N.A.
STRAIN=SJL/J, and B10.S/J; TISSUE=Spleen;
MA R. 2., Teuscher C.;
"Screening for candidate genes of mouse autoimmune diseases.";
Screening for Layer the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                    TISSUE-Uterus;
MEDLINE=91042558; PubMed=2484714;
White R., Lees J.A., Needham M., Ham J., Parker M.;
"Structural organization and expression of the mouse estrogen
                 01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha)
Name=E8rl; Synonyms=Nr3al, ESR, Estr, Estra;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575.
MEDLINE-21124487; Pubmed=11226831;
01-FBB-1991 (Rel. 17, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                  . Endocrinol. 1:735-744(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-22 FROM N.A. STRAIN=C57BL/6J; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ture 420:563-573 (2002)
                                                                                                  (Mouse)
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                             Mus musculus
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DAMA-binding domain and a C-terminal steroid-binding domain.
-!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).
-!- MISCELLANEOUS: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to receptor affinity. The hormone-receptor complex appears to receptor affinity. The sequences upstream of transcriptional start sites.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 275:13510-13516(2000).
-!- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGIL1352467; EST1.

R MGD; MGIL1352467; EST1.

R GO; GO:0005737; C:cytoplasm; IDA.

GO; GO:0005634; C:cnucleus; IDA.

GO; GO:0005634; C:nucleus; IDA.

GO; GO:0005634; C:nucleus; IDA.

R GO; GO:0005634; C:nucleus; IDA.

R GO; GO:00030235; F:nitric-captor activity; ISS.

R GO; GO:00030235; F:nitric-captor scipnaling pathway; ISS.

R GO; GO:0004694; P:cell growth; NAS.

GO; GO:0006355; P:negulation of transcription, DNA-dependent; ISS.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.

R InterPro; IPR001292; Obstrgn_receptor.

R InterPro; IPR001293; Stdhrmn_receptor.

R InterPro; IPR001323; Stdhrmn_receptor.

R InterPro; IPR001324; Stdhrmn_receptor.

R InterPro; IPR001324; Cat_ncl_receptor.
                                                                                                     MEDLINE-97336097; PubMed-9192892;
Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in target tissues.
SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Interacts with NCOA5. Binds UBEIC (By similarity).
                                                                                                                                                                                                                                                                                                                                          "Isolation and characterization of peroxisome proliferator-activated receptor (PPAR) interacting protein (PRIP) as a coactivator for
                                                                                                                                                                                                                                                                          MEDLINE=20250907; Pubmed=10788465;
Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
                                                                                                                                                                  "The transcriptional co-activator p/CIP binds CBP and mediates
                  "Glycosylation of the murine estrogen receptor-alpha.";
J. Steroid Biochem, Mol. Biol. 75:147-158(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M38651; AAA37580.1; -.
                                                                                                                                                                                           nuclear-receptor function.";
Nature 387:677-684(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlycoSuiteDB; P19785; -.
                                                                                 INTERACTION WITH NCOA3
                                                                                                                                                                                                                                                        INTERACTION WITH NCOA6
Cheng X., Hart G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A40061, ORMSE.
HSSP; P03372; 1HCP.
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                                                                                                                                                                                                                                                                                                                            Reddy J.K.;
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SEQUENCE FROM N.A.
  309 SPALSLTADQWVSALLDAEPPMIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV 368
                                                                                                                                                                                                                                                                                                                              61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLPAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                                                                                                                                                                                                    FDMLLATSSRFRWMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                                                                                                                                            TLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEML 548
                                                                                                                                                                                                                                                                                                                                                                                 TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                     1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1988 (Rel. 06, Last annotation update)
01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name=Esrl; Synonyma=Nr3al, Esr, Estr;
Rattus norvegicus (Rar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mannalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                  Phosphoserine (by CDK2) (By similarity)
Phosphoserine (by CDK2) (By similarity)
Phosphoserine (By similarity)
Phosphoserine (by CK2) (By similarity)
Phosphotyrosine (by Tyr-kinases) (By
                                                                                                                                                                                                                                                                           1,
                                                                                                                                                                                                                                                            DB 1; Length 599;
                                                                                                                                                                                                                                                           Score 1204.5; DB 1; Length
Pred. No. 1.5e-92;
5; Mismatches 3; Indels
                                                                                                                                                                                              O-linked (GlCNAc).
O-linked (GlCNAc).
O-linked (GlCNAc).
FTId=CAR_O00137.
F -> Q (in strain SJL/J).
L -> M (in Ref. 4).
                                                                                                                                                                                                                                             05F5E2FC21CC0A8B CRC64;
                                                                                                                                    Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 AA
                                                                                                                                                                                         similarity
                                                                                                                                             Poly-Ala.
                                                                                                               C4-type.
                                                                                                                             Hinge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
InterPro, IPR001628; Znf C4steroid
      Pfam; PF00104; Hormone recep; 1.
Pfam; PF02159; Oest recep; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                             66955 MW;
                                                                                                                                                                                                                                                            96.4%;
                                                                                                                                                                                                                                                                         Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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269
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575
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599 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                             DAHRL 553
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                                                                                                      DNA BIND
ZN FING
ZN FING
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CARBOHYD
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RA Furnel-Instance 1. Dong X., Bailey J.A., Reed C.A., Osborne E., Gize E.A., Ra Fundel-Instance 1. Dong X., Bailey J.A., Reed C.A., Osborne E., Gize E.A., Rix E.A., Bigsby R.M., Nephew K.P.; The standard cactivating enzyme of NEDDB inhibits steroid receptor function."; Mol. Endocrinol. 16:315-330(2002)

-1- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

CC r. SUBDINI: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes (By Similarity). Binds UBEIC.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- SUBCELLULAR LOCATION: Nuclear.

-1- DOMAIN: Composed of three domains: a modulating N-terminal domain.

-1- PTM: Phosphorylated by cyclin A/COR2 (By similarity).

-1- PTM: Phosphorylated by cyclin A/COR2 (By similarity).

-1- THIS PRELIANEOUS: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components;

-1- MISCELLANEOUS: In the absence of ligand, steroid hormone receptor receptor complex appears to recognize discrete DNA sequences

-1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
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                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=87174780; PubMed=3031601;
Koike S., Sakai M.;
"Molecular cloning and characterization of rat estrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGD; 2581; EST.;

GO; GO:0016049; P:cell growth; ISS.

GO; GO:0045839; P:negative regulation of mitosis; ISS.

InterPro; IPR000139; Hrmon receptor.

InterPro; IPR001292; Ocetrgn receptor.

InterPro; IPR001723; Stdhrmn_receptor.

InterPro; IPR008946; Str ncl receptor.

InterPro; IPR008946; Str ncl receptor.

FEm; PF00104; Hormone recep; 1.

Pfam; PF00105; Cost_recep; 1.
                                                                            Submitted (MAR-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 15:2499-2513(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; TISSUE=Uterus;
Maggi A.M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0543; OESTROGENR.
PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PROD00035; ZAF_C4steroid; 1.
SMART; SM00430; ADLI; 1.
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EMBL; X61098; CAA43411.1; -.
PIR; S07379; QRRTE.
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TRANSFAC; T00258; -.
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SEQUENCE FROM N.A.
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STRAIN=Wistar;
                                              Muramatsu M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 FDMLLATSSRFRMMILQGEEFVCLKSIILLINSGVYTFLSSTLKSLEEKDHIHRVLDKIND 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 TLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEML 549
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PUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).
SUBBURIT: Binds DNA as a homodimer. Can form a heterodimer with BSR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
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                                                                                                                                                                                                                                                                                                      Phosphoserine (by CDK2) (By similarity). Phosphoserine (by CDK2) (By similarity). Phosphoserine (By similarity). Phosphoserine (by CK2) (By similarity). Phosphotyrosine (by Tyr-kinases) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 45, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name-ESR1; Synonyms=NR3A1, ESR;
Estrogen receptor (ER)
Name-ESR1; Synonyms=NR3A1, ESR;
Sus scrofa (Pig)
Estrogen (Pig)
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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MEDLINE=95080454; PLDMed=7988744;
MEDLINE=95080454; D., Jungblut P.W., Thole H.H.;
Boekenkamp D., Jungblut P.W., Thole H.H.;
"The C-terminal half of the porcine estradiol receptor contains of the crementational modification: determination of the primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 600;
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                       DNA-binding; Nuclear protein; Phosphorylation; Receptor; Steroid-binding; Transcription regulation; Zinc-finger. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N -> T (in Ref. 3).
C9C7D8CACEOF57D8 CRC64;
                                                                                                              Nuclear receptor-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1200.5; DB : Pred. No. 3.2e-92;
                                                                                                                                                                                                                       Steroid-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                          Poly-Ala.
PS00031; NUCLEAR RECEPTOR; 1
                                                                                                                                                                   C4-type.
                                                                                                                                                                                                                                                                                 Poly-Ser
                                                                                                                                           C4-type.
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95.9%;
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                     SUBCELLULAR LOCATION: Nuclear.

DOWAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

FIN: Phosphorylated by cyclin A/CDK2 (By similarity).

MISCELLANEOUS: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
a strong increase of transcription of target genes. Binds UBEIC
                                                                                                                                                                                                                                                                                                                                  PROSITE; PS0031; NUCLEAR RECEPTOR; 1.
Direct protein sequencing; DNA-binding; Nuclear protein;
Phosphorylation; Receptor; Steroid-binding; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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(By similarity).
(by CK2) (By similarity).
'-inages) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoserine (by CDK2) (By similarity)
Phosphoserine (by CDK2) (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear receptor-type.
C4-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 95.8%; Score 1197.5; DB 3 Best Local Similarity 95.1%; Pred. No. 5.7e-92; Matches 233; Conservative 7; Mismatches 4
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Steroid-binding.
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PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM: PD000035; Znf C4steroid; 1.
SMART; SM00430; HOLL; 1.
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              (By similarity
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PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphoserine (by CDK2) (By similarity).
Phosphoserine (by CDK2) (By similarity).
Phosphoserine (by Similarity).
Phosphoserine (by KZ) (By similarity).
Phosphotyrosine (by Tyr-kinases) (By Similarity).
QL -> PF (in Ref. 2).
GV -> EVEQI (in Ref. 2).
GV -> KG (in Ref. 2).
R GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
R GO; GO:0016049; P:cell growth; ISS.
R GO; GO:0016049; P:cell growth; ISS.
R GO; GO:0045839; P:negative regulation of mitosis; ISS.
R GO; GO:00645839; P:negative regulation of mitosis; ISS.
R GO; GO:00645839; P:negative regulation of mitosis; ISS.
R GO; GO:00645839; P:negative regulation of mitosis; ISS.
R InterPro; IPR000336; Hrmon recept.
R InterPro; IPR001323; Stdhrmn recept.
R InterPro; IPR001323; Stdhrmn recept.
R InterPro; IPR00149; Str_ncl_recept.
R INTE; RR00149; GESTROGENR.
R RINTS; PR00147; STRODENNONER.
R RNART; SM00430; HOLI; L
R SMART; SM00430; HOLI; L
R SMART; SM00430; MOLI; L
R SMART; S
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T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00031, NUCLEAR RECEPTOR, 1.
DNA-binding; Nuclear profein; Phosphorylation; Receptor; Steroid-binding; Transcription regulation; Zinc-finger. DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E4D803B4FFDB257E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear receptor-type.
C4-type.
C4-type.
Hinge.
Steroid-binding.
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poly-Pro.
Poly-Ser.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
290
595 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAHRL 244
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ZN_FING
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SEQUENCE
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MOD_RES
MOD_RES
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                              FDMLLATSSRFRMMNLQG-EFVCLKSIILLINSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                        TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                     Ambitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).

- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Binds UBEIC (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain. SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 98-291 FROM N.A.
Jones J.E., Carpenter C.D., Lubbers L.S., Petersen S.L., Wade G.N.,
"Return of lordosis after food deprivation and refeeding in Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhat H.K., Vadgama J.V.; "Hamster estrogen receptor cDNA: cloning and mRNA expression."; J. Steroid Biochem. Mol. Biol. 72:47-53(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRI_MESAU STANDARD; PRT; 595 AA.
090225; 090206;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
01-007-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name=ESR1; Synonymm=NR3A1, ESR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P03372; 1HCQ.
GO; GO:0016585; C:chromatin remodeling complex; ISS.
GO; GO:0016020; C:membrane; ISS.
GO; GO:0030284; F:estrogen receptor activity; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20197937; PubMed=10731637;
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NCBI_TaxID=9796;
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ZN FING
ZN FING
 299 SPALSLTAEQMVSALLEAEPPIVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRV 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLIHLMAKAGLTLÖQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                  Sumida K., Ooe N., Saito K., Kaneko H.;
"Molecular cloning and characterization of reptilian estrogen receptor
                                                                                                                                                                                                                                               R GO; GO:0016585; C:chromatin remodeling complex; ISS.

R GO; GO:0016585; C:membrane; ISS.

R GO; GO:0016585; C:membrane; ISS.

R GO; GO:0030235; F:nitric-oxide synthase regulator activity; ISS.

R GO; GO:003025; F:nitric-oxide synthase regulator activity; ISS.

R GO; GO:003025; F:nitric-oxide synthase regulator activity; ISS.

R GO; GO:003025; F:nitric-oxide synthase regulator activity; ISS.

R GO; GO:000355; F:nitric-oxide synthase regulator, DNA-dependent; ISS.

R InterPro; IPR001292; Oestrgn_receptor.

R InterPro; IPR001292; Oestrgn_receptor.

R InterPro; IPR001294; Strind_receptor.

R Ffam; PF00159; Oest. recep; 1.

R Ffam; PF00105; zf-C4; 1.

R PRINTS; PR00047; STROIDFINGER.

R PRINTS; PR00047; STROIDFINGER.

R PRINTS; PR00047; STROIDFINGER.

R PROMOR PROMORS; IRC C4; 1.

R MARRT; SM00399; ZnF_C4; 1.
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                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Caiman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
-1- SUBLETLY: Belongs to the nuclear hormone receptor family.
EMBL; AB055220; BAB79436.1; --
HSSP; P03372; 1HCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 94.4%; Score 1179.5; DB 2; Length Best Local Similarity 93.9%; Pred. No. 1.8e-90; Matches 230; Conservative 11; Mismatches 3; Indels
                           Caiman crocodilus (Spectacled caiman) (Caiman sclerops)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear procein; Receptor;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 587 AA; 66513 WW; DE1FP2B83FFCF913 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          594 AA
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(Rel. 40, Last sequence update)
                                                                                                                                                                            Cell. Endocrinol. 183:33-39(2001).
                                                                                                 SEQUENCE FROM N.A. MEDLINE=21490797; Pubmed=11604222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                         NCBI_TaxID=8499;
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ESRI HORSE
1D ESRI HORSE
AC Q9TV98;
DT 16-OCT-2001 (
DT 16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                     (By similarity).
--- SUBCELJULAR LOCATION: Nuclear.
--- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
--- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
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R HSSP; P03372; HGCP.

R GO; GO:0016585; C:chromatin remodeling complex; ISS.

R GO; GO:0016585; C:chromatin remodeling complex; ISS.

R GO; GO:0030235; F:nitrio-coxide synthase regulator activity; ISS.

R GO; GO:0030235; F:nitrio-coxide synthase regulator activity; ISS.

R GO; GO:0016049; P:cell growth; ISS.

R GO; GO:0016049; P:cell growth; ISS.

R GO; GO:0016049; P:negative receptor signaling pathway; ISS.

R GO; GO:0016049; P:negative receptor signaling pathway; ISS.

R GO; GO:001635; P:negative receptor.

R CO; GO:001635; P:regulation of transcription, DNA-dependent; ISS.

R THCEPTO; IPR001723; RTM-receptor.

R INTERPO; PR001929; ZH_C4FECOTO.

R Ffam; PR00104; HORMONE_RECEPTOR.

R PRINTS; PR001059; ZH_C4FECOTO.

R PRINTS; PR001099; ZTRDIPEINGER.

R PRINTS; PR001099; ZTRDIPEINGER.

R PRINTS; RR0047; STROIDFINGER.

R PRINTS; RR00430; HOLEAR RECEPTOR; I.

R RNART; SM00430; HOLEAR RECEPTOR; I.

R RNART; SM0039; ZHF C4; I.

R RNART; RN00410; HOLEAR RECEPTOR; I.

R RNART; RN00410; HOLEAR RECEPTOR; I.

R RNART; RN00410; HOLEAR RECEPTOR; I.

R RNART; RN0410; R
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                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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DOMAIN 1 184 Modulating.
01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha)
Mame-ESR1; Synonyma-NR3A1, ESR;
Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear receptor-type.
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C4-type.
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similarity).

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587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAHRL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAHRL 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHICK
                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                           DNA BA
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ESR1_CHICK
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                                                                                           SPVLSLTAEQMISALLDAEPPVLYSEYDATRPFNEASMMGLLTNLADRELVHMINWAKRV 364
                                                                                                                                PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                              FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                    TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                                                  FDMLLAISSRLRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKMTD 484
                                                                                                                                                                                                                                                       485 TLIHLMAKAGLTL-QQHRRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 543
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                                                                            1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Hypothalamus;
MEDLINE=97163508; PubMed=9010328;
Jacobs E.C., Arnold A.P., Campagnoni A.T.;
Labra finch estrogen receptor CDNN: cloning and mRNA expression.";
I. Steroid Biochem. Mol. Biol. 59:135-145(1996).
I. FUNCTION: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.
-!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with BR-berea (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.

DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; (Taeniopygia guttata).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Estrildidae;
NCBI TaxTh-co-raiopygia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0016585; C:chromatin remodeling complex; ISS.
GO:0016020; C:membrane; ISS.
GO:0030284; F:estrogen receptor activity; ISS.
GO:0030235; F:nitric-oxide synthase regulator activity; ISS.
                                                     7
                            Length 594;
                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha)
 DD36CA7C24C74B95 CRC64;
                          1;
                        Score 1179; DB 1
Pred. No. 2e-90;
                                                                                                                                                                                                                                                                                                                                                                                     587 AA
                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
 66103 MW;
                        94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L79911; AAB81108.1; -. HSSP; P03372; 1HCP.
                                                    Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
  594 AA;
                                       Similarity
                                                                                                                                                                                                                                                                                         DAHRL 244
                                                                                                                                                                                                                                                                                                                   DAHRL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily
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SEQUENCE
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                          Query Match
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                                       Local
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ESR1_POEGU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krust A., Green S., Argos P., Kumar V., Walter P., Bornert J.-M.,
Chambon P.,
"The chicken oestrogen receptor sequence: homology with v-erbA and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                     DNA-dependent; ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86247578; PubMed=3755102;
Krust A., Green S., Argos P., Kumar V., Walter P., Bornert J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 587;
GO:0030520; P:estrogen receptor signaling pathway; ISS GO:0006355; P:regulation of transcription, DNA-depende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                           SMART; SM00399; ZNF C4; 1.
PROSITE; PS00031; NÜCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Steroid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name-ESR1; Synonyms-BRAA1, ESR;
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4-type.
Hinge.
Steroid-binding.
; 2B254168A7A910AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear receptor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;; Score 1177.5; DB
;; Pred. No. 2.7e-90;
12; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             589 AA
                                                                                                                                                                                                                                                                                                                                                                                               Modulating
                                    InterPro; IPR000536; Hrmon recept 119
InterPro; IPR001292; Oestrgn_receptor.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001946; Str ncl_receptor.
InterPro; IPR001628; Znf_C4sTeroid.
                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation, Zinc-finger
                                                                                                                                                                                                                                                                                                                                                                                                                                       C4-type
                                                                                                                                                                                                  PRINTS; PRO0543; OESTROGENR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; Znf C4steroid; 1.
SMART; SM00430; HOLI; 1.
                                                                                                                                         Pfam; PF00104; Hormone recep; 1. Pfam; PF02159; Oest recep; 1. Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66553 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.2%;
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Best Local Similarity 93.5%;
Matches 229; Conservative
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237
302
587
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299 SPALSLTAEQMVSALLEAEPPIVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRV 358
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359 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSVEHPGKLLFAPNLLLDRNGGKCVEGMVEI
                                                                                   TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A runwell-1498003;

A cates Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S., Gunderson M.P., Kohno S., Bryan T.A., Guillette L.J., Iguchi T.;

"Wolecular cloning of the estrogen and progesterone receptors of the merican alligator.";

"Wolecular cloning of the estrogen and progesterone receptors of the survival state of the substance of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alligator mississippiensis (American alligator).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Crocodylidae, Alligatorinae, Alligator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 587;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                      587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, TrEMBLrel. 27, TrEMBLrel. 27,
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                                                                                                                                                                                                                                                   539 DAHRL 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=14980803;
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05-JUL-2004
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05-JUL-2004
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                                    419
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation has buropean Bioinformatics institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  EMBO J. 5:891-897(1986).

-!- FUNCTION: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

-!- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-
                                                                                                                                                         -:- SUBCELLULAR LOCATION: Nuclear.
-:- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal seroid-binding domain.
-:- MISCELLANEOUS: In the absence of ligand, steroid-binding domain.
-:- Another to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor omplex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
-:- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO: GO: 0016585; C:chromatin remodeling complex; ISS.

R GO: GO: 0016200; C:membrane; ISS.

R GO: GO: 0010284; F:estrogen receptor activity; ISS.

R GO: GO: 0030235; F:nitric-oxide synthase regulator activity; ISS.

R GO: GO: 0030235; F:nitric-oxide synthase regulator activity; ISS.

R GO: GO: 0030235; F:nitric-oxide synthase regulator activity; ISS.

R GO: GO: 0006355; F:regulation of transcription, DNA-dependent; ISS.

R InterPro; IPR000536; Hrmon receptor.

R InterPro; IPR001292; Oestrgn receptor.

R InterPro; IPR001592; Cestrgn receptor.

R InterPro; IPR001628; Stf_G4sTeroid.

R Pfam; PF001159; Oest recep; 1.

R Pfam; PF001159; Cest recep; 1.
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DNA-binding; Nuclear protein; Receptor; Steroid-binding;
Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 Steroid-binding.
66746 MW; 1B092233C770A54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear receptor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.1%; Score 1176.5; DB 1
llarity 93.5%; Pred. No. 3.3e-90;
Conservative 12; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating
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C4-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0543; OESTROGENR.
PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
ProDom; PD000035; Znf C48teroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X03805; CAA27433.1; -. PIR, A40914; QRCHE. HSSP, P03372; 1HCP. TRANSFAC; T00264; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ω.
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IART; SM00399; ZNF_C
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215
245
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589 AA;
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ZN FING
ZN FING
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        SEQUENCE FROM N.A.
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TISSUE-Uterus;
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           239
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Estrogen receptor alpha.
Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERA.
Alligator mississippiensis (American alligator).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Crocodylidae, Alligatorinae, Alligator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Katsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S., Gunderson M.P., Kohno S., Bryan T.A., Guillette L.J., Iguchi T.; "Molecular cloning of the estrogen and progesterone receptors of American alligator.";
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                                                                                                                                                                                                                                                                                                                                                                     14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.0%; Score 1175.5; DE 93.5%; Pred. No. 4e-90; ive 12; Mismatches
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EMBL; AB115909; BAD08348.1; -.
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Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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BAD08348;
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                                                                                                                                                             R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005496; F:steroid binding; IEA.

GO; GO:0005496; F:steroid binding; IEA.

GO; GO:0003700; F:steroid hormone receptor activity; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001295; Hrmon recept lig.

R InterPro; IPR001295; Cestrgn_receptor.

R InterPro; IPR00123; Stdhmn_receptor.

R InterPro; IPR001529; Str_ncl_receptor.

R InterPro; IPR001628; Znf_C4steroid.

R Ffam; PF00104; Hormone_recept.

R Pfam; PF00144; Hormone_recept.

R Pfam; PF001459; Oest recept.

R Pfam; PF001658; Zf_C4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FDMLLATAARFRAMILQGEEFVCLKSIILLNSGVYFFLSSTLKSLEERDYIHRVLDKITD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NÜCLEAR_RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE S89 AA; 66767 WW; 8271FDAA65552CA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23, Created)
23, Last sequence update)
26, Last annotation update)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.1%; Score 1172.5; DB 93.1%; Pred. No. 7.1e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PROD543; OESTROGENR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PROD00035; EAF_C4steroid; 1.
SMART; SM00399; ZAF_C4; 1.
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01.MAR-2004 (TrEMBLrel. 26
Estrogen receptor alpha (F.
Name=ESR1;
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242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 PGFGDLTLHDQVHLLECAWLEILMIGLIWRSWEHPGKLLFAPNLILDRNQGKCVEGMVEI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FDWLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang X., Harris H.;

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

-!- SUNCELLUIAR LOCATION: Nuclear (By similarity).

-!- SIMILARIY: Belongs to the nuclear hormone receptor family.

R G0; G0:000370; P:steroid hormone receptor activity; IEA.

G0; G0:000370; F:steroid hormone receptor activity; IEA.

G0; G0:000370; F:steroid hormone receptor activity; IEA.

G0; G0:000370; F:steroid hormone receptor activity; IEA.

G0; G0:000370; F:transcription factor activity; IEA.

G0; G0:000355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000356; Hrmon receptor.

InterPro; IPR00356; Str ncl_receptor.

R InterPro; IPR00368; Str ncl_receptor.

R InterPro; IPR00368; Str ncl_receptor.

R Pfam; PF00104; Hormone recept) 1.

R Pfam; PF00104; Hormone recept) 1.

R Pfam; PF00104; Hormone recept) 1.

R Pfam; PF00104; Hormone receptor 2.

R Pfam; PF00104; Hormone receptor 3.

R Pfam; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 FDMLLATSTRFRWMNLQGEEFVCLKSIILLNSGMYFFLSSTLKSLEEKDHIHRVLDKIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%; Score 1170.5; DB 2; Length 353; 92.7%; Pred. No. 5.8e-90; tive 12; Mismatches 5; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: November 8, 2004, 08:27:59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 93.6%
Best Local Similarity 92.7%
Matches 227; Conservative
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303 EAHRL 307
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

November Run on:

8, 2004, 08:14:27; Search time 11.951 Seconds (without alignments) 1964.426 Million cell updates/sec

US-09-830-693B-27

1250 1 SLALSLTADOMVSALLDAEP......CKNVVPLYDLLLEMLDAHRL 244 Perfect score: Sequence:

**BLOSUM62** 

Scoring table:

Gapop 10.0 , Gapext 0.5 Searched:

283416 segs, 96216763 residues

number of hits satisfying chosen parameters:

283416

length: 0 length: 2000000000 Bed Bed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	IB estrogen receptor	estrogen	estroden			esti	estrogen	estrogen	oestrogen		estrogen	estrogen	estrogen		119 estradiol receptor		187 estrogen receptor		86 glucocorticoid rec									Cicuitar
C)	a	ORHUE	ORMSE	ORRTE	147140	864737	QRCHE	ORXLE	T10423	S58224	A37197	871400	JC5939	JW0046	S26595	167419	B29345	S58087	A29345	860586	A25923	QRHUP	A43781	A35466	A39596	153280	150515	C41977	826670
	DB	;	٦	•	7	•	٦	-	~	7	•	~	•	7	7	~	~	•••	•••	7	•	Н						~	N
	Query Match Length	595	599	909	595	701	589	586	620	535	574	477	530	503	133	121	433	433	521	758	930	933	467	786	923	923	441	488	463
, ako	Query Match	98.4	96.4	96.0	92.8	94.2	94.1	85.3	64.4	63.8	62.0	8.09	60.8	59.7	52.8	46.4	29.3	27.7	24.7	20.8	20.0	19.9	19.8	19.7	19.7	19.6	19.4	19.2	19.1
	Score	1230.5	1204.5	1200.5	1197.5	1177.5	1176.5	1066.5	804.5	797.5	774.5	759.5	759.5	746.5	659.5	580.5	366.5	346.5	309	260.5	250	249	247.5	246.5	246	245	242	240.5	238.5
	Result No.		8	m			Ĵ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28

retinoid X recepto	retinoic acid rece	retinoid X recepto	retinoid receptor	glucocorticoid rec	retinoid X recepto	retinoid X recepto	retinoic acid rece	H-2 region II bind	retinoid X recepto	retinoic acid rece	RXR-betal isoform	glucocorticoid rec	glucocorticoid rec	androgen receptor	glucocorticoid rec
109592	S26668	47278	D41977	A54273	150514	S37781	S26669	A34418	D41727	A41651	184718	QRHUGA	A25691	JG0194	QRHUGB
Š	S	•													
7	2 S	7	~	~	N	N	N	N	N	~	~	-	Н	~	-
-	467 2 S	N	470 2	771 2	379 2	533 2	410 2	446 2	448 2	451 2	520 2	1777	783 1	848 2	742 1
462 1	7	18.9 467 2	18.6	18.4	18.3	18.0	17.9	17.9	17.9	17.9	17.9				
18.9 462 1	467 2	18.9 467 2	18.6		18.3	18.0	17.9	17.9	17.9	17.9	17.9	17.9		17.9	17.8

## ALIGNMENTS

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RESULT 1
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- human receptor 1

NiAlternate names: ER1; estrogen receptor alpha (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004 (Species: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004 (Species: 28-May-1986 #sequence, Alional Species: Alion

A; Accession: A94284

A; Molecule type: mRNA A; Residues: 1-595 <GR1>

A)Cross-references: UNIPROT:Q14268; UNIPROT:Q9UE35; GB:M12674; NID:g182192; PIDN:AAA5239 R)Cross-references: UNIPROT:Q14268; UNIPROT:Q9UE35; GB:M12674; NID:g182192; PIDN:AAA5239 R)Creen, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P. Alatres 320, 114-119, 1189; PISS A)Title: Human oestrogen receptor CDNA: sequence, expression and homology to v-erb-A. A)Reference number: A93376; MUID:86146892; PMID:3754034

A;Cross-references: GB:X03635; NID:g31233; PIDN:CAA27284.1; PID:g31234 R;Ponglikitmongkol, M.; Green, S.; Chambon, P. EMBO J. 7, 3385-3388, 1988 A;Accession: A93376 A;Molecule type: mRNA A;Residues: 1-595 <GR2>

A;Title: Genomic organization of the human oestrogen receptor gene. A;Reference number: A43021; MUID:89091079; PMID:3145193

A, Accession: A43021
A, Molecule type: DNA
A, Residues: 143-161,205-225;244-264;356-374,'G',376;402-422;447-460,'P',462-467;508-528
R, Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992
A, Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
A, Reference number: S27140; MUID:93075998; PMID:1476547

A, Accession: S27143 A, Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-115 <KEA>

A;Cross-references: EMBL:X62462; NID:g31201; PIDN:CAA44322.1; PID:g31205 R;Pfeffer, U.; Fecarotta, E.; Castagnetta, L.; Vidali, G. Cancer Res. 53, 741-743, 1993

A,Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive h A,Reference number: S34000, MUID:93153765; PMID:7916651

A; Accession: S34000

A;Status: preliminary

A; Molecule type: mRNA A; Residues: 216-254,367-399,'G',401-434 < PFE> A; Cross-references: EMBL:X73067; NID:9579865; PIDN:CAA51528.1; PID:9939886 A; Note: the authors translated the codon GGG for residue 400 as Val R; Dotalaw, H.; Alkhalaf, M.; Murphy, L.C. Mol. Endocrinol. 6, 773-785, 1992 A; Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.

1;

Gaps

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9

428

488 239

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C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly & complex appears to recognize discrete DNA sequences upstream of transcriptional start site C;Superfamily: estrogen receptor; enb transforming protein homology c;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor F;1-189/Domain: amino-terminal kHi2>
F;184-275/Domain: amino-terminal kHi2>
F;187-460/Domain: enh transforming protein homology <ERBA>
F;187-460/Domain: erbA transforming protein homology <ERBA>
F;187-460/Domain: arinc finger CCC motif F;22-245/Region: zinc finger CCC motif F;22-245/Region: zinc finger CCC motif F;260-275/Region: steroid binding #status predicted <STB>
F;280-375/Region: steroid binding #status predicted F;251,241,244/Binding site: zinc (Cys) #status predicted F;251,241,244/Binding site: zinc (Cys) #status predicted F;240,309/Binding site: zinc (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S16731
A;Reference number: S16731
A;Residues: 1.487,7T',489-600 cMAG>
C;Comment: The steroid hormones and their receptors are involved in the regulation of eul C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly is cmplex appears to recognize discrete DNA sequences upstream of transcriptional start site C;Superially: estrogen receptor; enbA transforming protein homology
C;Reywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor F;188-461/Domain: DNA binding protein homology cERBA>
F;188-461/Domain: erbA transforming protein homology cERBA>
F;188-461/Domain: ainc finger CCCC motif
F;224-246/Region: zinc finger CCCC motif
F;261-276/Region: nuclear location signal
F;305-557/Domain: steroid binding #status predicted cSTB>
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Cispecies: Rattus norvegicus (Norway rat)
Cipate: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cipate: 30-Sep-1991 #sequence revision 14-Jul-1994 #text_change 09-Jul-2004
Nucleic Acids Res. 15, 2499-2513, 1987
Nucleic Acids Res. 15, 2499-2513, 1987
A;Ritle: Molecular cloning and characterization of rat estrogen receptor cDNA.
A;Recession: S07379
A;Molecule type: mRNA
A;Residues: 1-600 <KOI>
A;Crossion: S07379
A;Molecule type: WRNA
A;Residues: 1-600 <KOI>
A;Crossion: UNIPROT:P06211; EMBL:Y00102; NID:G56110; PIDN:CAA68287.1; PID:G56111
SNAMG931, A.M.A.
Submitted to the EMBL Data Library, June 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      489 TLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1204.5; DB 1; Length
Pred. No. 2.4e-96;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.4%;
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Best Local S
Matches 236
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A; CDB:ESR1; ESR
A; CDB:ESR1; 254/1; 366/1; 412/2; 457/1; 518/2
A; Introns: 151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2
C; Superfamily: estrogen receptor; erbA transforming protein homology
C; Keywords: DNA binding; nucleus; phosphoprotein; steroid hormone receptor; transcriptic
C; Keywords: DNA binding; nucleus; prosphoprotein; steroid hormone receptor; transcriptic
C; Keywords: DNA binding #status predicted <DNA>
F;121-299/Domain: maino-terminal protein homology <ERBA>
F;181-456/Domain: sinc finger CCCC motif
F;221-245/Region: zinc finger CCCC motif
F;230-595/Domain: steroid binding #status predicted
F;236,305/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strongen receptor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A,Title: Structural organization and expression of the mouse estrogen receptor.
A,Reference number: A40061; MUID:91042558; PMID:2484714
A,Accession: A40061
A,Accession: A40061
A,Residues: 1-599 <AMID
A,Residues: 1-599 <AMID
A,COMMENT: The steroid hormones and their receptors are involved in the regulation of ev
                                                                                                      A,Molecule type: mRNA

A,Residues: 1-214, ELPTLC, <DOT>
A,Residues: 1-214, ELPTLC, <DOT>
A,Experimental Source: Clone 4; breast cancer
A,Experimental source: clone 4; breast cancer
A,Note: sequence has been revised after extraction from NCBI backbone
A,Note: complete sequence of neither the nucleotide nor the protein is shown in this A,Note: extracted from NCBI backbone (NCBIN:106580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Comment: The steroid hormones and their receptors are involved in the regulation of eu C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly omplex appears to recognize discrete DNA sequences upstream of transcriptional start sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364
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A;Reference number: A41925; MUID:92293154; PMID:1603086
A;Accession: A41925
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Pred, No. 1.3e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Cross-references: GB:M69296
A)Experimental source: clone 24; breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                            Status: significant sequence differences
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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A,Cross-references: EMBL:U47678; NID:g1197854; PIDN:AAB00115.1; PID:g1197855
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ripink, J.J.; Wu, S.Q.; Wolf, D.M.; Bilimoria, M.M.; Jordan, V.C.
Nucleic Acids Res. 24, 962-969, 1996
A; Fittle: A novel 80 kDa human estrogen receptor containing a duplication of exons a streamnen number: S64737; MUID:96174665; PMID:8600466
A; Accession: S64737
A; Extures preliminary; nucleic acid sequence not shown; translation not shown a; Molecule type: mRNA
A; Residues: 1-701 < PIN>
                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                        179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                      SPULSLIADOMISALLEAEPPIIYSEYDPTRPLSEASWMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                             PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                               365 PGFLDLSLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                        FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD
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                                                                                                                       1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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              Length 595;
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                                                                    Indels
           Score 1197.5; DB 2;
Pred. No. 9.5e-96;
7; Mismatches 4; 1
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              95.8%;
                                          95.1%;
                                                                 Conservative
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Matches 243; Conservative
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                                       Similarity
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                                                                 Matches 233;
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                                             Best Local
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: 1-595 <BOK>
A.Cross-references: UNIPROT:Q29040; EMBL:Z37167; NID:g58754; PIDN:CAA85524.1; PID:g5875
A.Stylole, H.H.; Maschler, I.; Jungblut, P.W.
Eur. J. Biochem. 231, 510-516, 1995
A.T. S. Surface mapping of the ligand-filled C-terminal half of the porcine estradiol reference number: S66250; MUID:95361877; PMID:7635163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCEBBION: 332402
A, Molecule type: protein
A, Molecule type: protein homology
C, Keywords: DNA binding #status predicted <DNA>
F, 120, Domain: maino-terminal total
F, 121, 299, Domain: bNA binding #status predicted <DNA>
F, 185-205, Region: zinc finger CCCC motif
F, 221, 245, Region: nuclear location signal
F, 300-595, Domain: steroid binding #status predicted
F, 221, 225, Domain: steroid binding #status predicted
F, 221, 227, 237, 240, Binding site: zinc (Cys) #status predicted
F, 236, 305, Binding site: zinc (Cys) #status predicted
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A;Title: Assignment of the ligand binding site of the porcine estradiol receptor to the
A;Reference number: S32402; MUID:93209384; PMID:8458437
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                                                                                                                                                                                                                                                                             310 SPALSLTADOMVSALLDAEPPLIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV 369
                                                                                                                                                                                                                                                                                                                                PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     estradiol receptor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I47140; S66250; S3402
R;Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.
MOI. Cell. Endocrinol. 104, 163-172, 1994
A;Fitle: The C-terminal half of the porcine estradiol receptor contains no FA;Reference number: I47140; MUID:95080454; PMID:7988744
                                                                                                                                                                                                                             SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML
                                                                                                                                                                          Gaps
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F;190,193,207,210/Binding site: zinc (Cys) #status predicted F;226,232,242,245/Binding site: zinc (Cys) #status predicted F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted
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A. A. Cestion: 866250; MUD:95361877; PMID:7635163
A. Molecule type: protein
A. Molecule type: protein
A. Residues: 297-307,310-313;320-323;337-340;417-420;466-473
A. Experimental source: uterus
R. Thole, H. H.
                                                                                                                                                                          1;
                                                                                                                 Score 1200.5; DB 1; Length 600;
Pred. No. 5.3e-96;
5; Mismatches 4; Indels 1;
                                                                                                              Query Match
Best Local Similarity 95.9%;
Matches 235; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554
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605 OQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRL 655

6 and

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R;Weiler, I.J.; Lew, D.; Shapiro, D.J.

Mol. Endocrinol. 1, 355-362, 1987

A;Title: The Xenopus laevis estrogen receptor: sequence homology with human and avian rec
A;Reference number: A40907; MUID:90331927; PMID:3274894

A;Reference number: A40907

A;Rodecule type: MRNA
A;Residues: 1-586 *WEINA
A;Residue: The steroid hormones and their receptors are thought to be weakly & C;Comment: The steroid hormones receptors complex appears to recognize discrete DNA sequences upstream of transcriptional start site
C;Superfamily: estrogen receptor; erbA transforming protein, steroid binding; steroid hormones recept
F;178-448/Domain: amino-terminal akH2>
F;178-448/Domain: amino-terminal akH2>
F;178-448/Domain: amino-terminal akH2>
F;178-448/Domain: amino-terminal protein homology cERBA>
F;178-266/Domain: are finger CCC motif
F;178-21-266/Region: ruclear location signal
F;251-266/Region: nuclear location signal
F;210-181,197,200/Binding site: zinc (Cys) #status predicted
F;211/Binding site: phosphate (Ser) (covalent) #status predicted
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C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation
F;184-460/Domain: erbA transforming protein homology <ERB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 SPVLSLTAEQLISALMEAEAPIVYSEHDSTKPLSEASMMTLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
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82.9%; Pred. No. 2e-84;
ive 26; Mismatches 15; Indels
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Albescription: Cloning of medaka estrogen receptor CDNA. Alvacession: T10423
Alvacesion: 
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Matches 203; Conservative
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Attents; precedences; predicted normone receptor; precedences; predicted normology
C; Comment: The steroid hormones and their receptors are involved in the regulation of eucic supperfamily; estrogen receptor; erbA transforming protein homology
C; Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor; erbA transforming protein homology cERBA>
F; 177-200/Region: zinc finger CCC motif
F; 213-215/Region: zinc finger CCC motif
F; 214-246/Domain: erbA transforming protein homology cERBA>
F; 214-246/Domain: erbA transforming protein homology cERBA>
F; 217-250/Domain: erbA transforming protein homology cERBA>
F; 218-246/Domain: erbA transforming protein homology cERBA>
F; 218-246/Domain: erbA transforming protein homology cERBA>
F; 218-246/Domain: erbA transforming protein homology cERBA>
F; 218-21, 234/Binding site: zinc (Cys) #status predicted
F; 230, 299/Binding site: zinc (Cys) (covalent) #status predicted
                                                                                                                                                                                                           estrogen receptor - chicken
Cispecies: Gallus gallus (chicken)
Cjate: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cjate: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cjacession: A40914; S07192
R;Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley,
MA). Endocrinol. 1, 25-35, 1987
A;Title: Structural organization and regulation of the chicken estrogen receptor.
A;Reference number: A40914; MUID:88318621; PMID:2901032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1.589 «MAX»
A; Cross-references: UNIXPOT: P06212
A; Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
EMBO J. 5, 891-897, 1986
A; The chicken oestrogen receptor sequence: homology with v-erbA and the human
A; Pence number: S07192; MUID: 86247578; PMID: 3755102
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Feb-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: A40914
A, Status: not compared with conceptual translation
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R;Pakdel, F.; Le Gac, F.; Le Goff, P.; Valotaire, Y.
Mol. Cell. Endocrinol. 71, 195-204, 1990
A;Title: Full-length sequence and in vitro expression of rainbow trout estrogen receptor A;Reference number: A37197; MUID:91006824; PMID:2210031
A;Accession: A37197
                                                                                                                                                                                                                                         A;Cross references: GB:M1559
R;Pakdel F: Le Guellec, C.; Vaillant, C.; Le Roux, M.G.; Valotaire, Y.
Mol. Endocrinol. 3, 44-51, 1989
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger
A;Title: Identification and estrogen induction of two estrogen receptors
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: ISO-374 cPA2>
A;Status: ISO-374 cPA2>
A;Cross-references: GB:M1559; NID:g213783; PIDN:AAA49552.1; PID:g213784
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Stypordia DNA binding; nucleus; steroid hormone receptor; transcription regulation; zir
F;145-421/Domain: erbA transforming protein homology cERBA>
F;147-167/Region: zinc finger
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R;Mosselman, S.; Polman, J.; Dijkema, R.
ERSE Lett. 392, 49-53, 1996
A;Title: ER-beta: identification and characterization of a novel human estrogen receptor A;Reference number: S71400; MUID:96354875; PMID:8769313
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A; Residues: 1-477 < MOS>
A; Residues: 1-477 < MOS
A; Residues: EMBL:X99101; NID:g1518262; PIDN:CAA67555.1; PID:g1518263
A; Residues: Except receptor; exbA transforming protein, steroid binding; steroid hormone receptor; Rey-4355/Damain: exbA transforming protein homology < RRBA>
F; 96-115/Region: zinc finger CCCC motif
F; 96-116/Region: zinc finger CCCC motif
F; 96-116/Region: zinc finger CCCC motif
F; 95-113/116/Binding site: zinc (Cys) #status predicted
F; 96, 99, 113, 116/Binding site: zinc (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               338
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C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 EQVLFILQGQTPALCSRQKVARPYTEVTWMTLITSMADKELVHMIAWAKKVPGFQELSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOVHILLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 RFRMMNLQ-GEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.0%; Score 774.5; DB 2; Best Local Similarity 63.1%; Pred. No. 3.6e-59; Matches 149; Conservative 39; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 60.8%; Score 759.5; DB 2; Best Local Similarity 59.5%; Pred. No. 5.7e-58; Matches 144; Conservative 56; Mismatches 37;
                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-574 <PAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S71400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
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C;Superfamily: estrogen receptor; exbA transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F:103-382/Domain: exbA transforming protein homology <ERBA>
                                                                                                                                 432
                                                                                                                                                                                                                 DLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDML 124
                                                                                                                                                                                                                                                                                                                                     LATSSRFRMMNLQ-GEFVCLKSIILLINSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIH 183
                                                                                                                                                                                                                                                                                                                                                                       LMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLBMLDAHR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNGGKCVEGMVEIFDM 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ocetrogen receptor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58224
R;Redersc S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T.
R;Reference number: S58224
A;Reference number: S58224
A;Reference number: S58224
A;Accession: S58224
A;Accession: S58224
A;Reference number: S58224
A;Residues: 1-535 - ROG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        estrogen receptor - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999
C;Accession: A37197; A40070
                                                                                                                                                                                                                                                     SLTADOMYSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFV
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                                                 Gaps
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                                              44; Indels
               Pred. No. 1e-61;
2; Mismatches
                                           42;
         63.9%;
               Best Local Similarity 63.9
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 62.8
Matches 152, Conservative
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RESULT 10

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A;Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in A;Reference number: JW0046, MUD:98262932; PMID:9600083
A;Accession: JW0046
A;Accession: JW0046
A;Residues: 1-503 < AMR>
A;Residues: 1-503 < AMR>
A;Cross-references: DDBJ.AB012721
C;Comment: This protein functions as a negative regulator of estrogen action.
C;Superfamily: estrogen receptor; erbA transforming protein homology
F;102-381/Domain: erbA transforming protein homology < ERBA>>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT: P49884; EMBL: X66841; NID: 9334; PIDN: CAA47317.1; PID: 9335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 QEAESSRKLTHILLNAVTDALVWVIAKSGISSQQQSVRLANILMILSHVRHISNKGMEHLL 450
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                                                                                                                                                                                                                                                                                                                                                                                                    271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LTLHDQVHLLECAMLEILMIGLVWRSMEHPVKLLFAPNLLLDRNQGKCVEGWVEIFDMLL
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                                                                                                                                                                                                                                                                                                                                                   2 LALSLIADOMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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-i
                                                                                                                                                                                                                                                          Length 503;
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                                                                                                                                                                                                                                                     59.7%; Score 746.5; DB 2;
56.3%; Pred. No. 8.1e-57;
iive 52; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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Pred, No. 5.3e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: $26595
R;Hagen-Mann, K.; Mann, W.; Meyer, H.H.D.
Bubmitted to the EMBL Data Library, May 1992
A;Reference number: $26595
A;Accession: $26595
A;Accession: $26595
A;Molecule type: mRNA
A;Residues: 1-133 < HAG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              estrogen receptor - bovine (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.5%;
Matches 131; Conservative
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                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.3<sup>†</sup>
Matches 148† Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
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JC5939
estrogen receptor beta - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JC5339
R;Ogawa, S; Inoue, S; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Murama Biochem. Biophys. Res. Commun. 243, 122-126, 1998
A;Title: The complete primary structure of human estrogen receptor beta (hERbeta) and it A;Reference number: JC5939; MUID:98139878; PMID:9473491
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.; Kat
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N;Alternate names: ERbeta2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
C;Accession: JW0046
R;Maruyama, K.; Endoh, H.; Sasaki-Iwaoka, H.; Kanou, H.; Shimaya, E.; Hashimoto,
Biochem. Biophys. Res. Commun. 246, 142-147, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: DDBJ:AB006590; NID:g2911151; PIDN:BAA24953.1; PID:g2911152
C;Superfamily: estrogen receptor; erbA transforming protein homology
F;147-408/Domain: erbA transforming protein homology <ERB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||:|||| : || |::||||:|||| 380 LLATTSRFRELKLQHKEYLCVKAMILINSSMYPLVTAT-QDADSSRKLAHLLNAVTDALV 438
                                                          266
                                                                                                           64 VDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNOGKCVEGMVEIFDM 123
                                                                                                                                    LLATSSRFRMMLLQ-GEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLI 182
                                                                                                                                                                                                                                        183 HLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAH 242
                                                                                                                                                                                                                                                                                                                                  386 WVIAKSGISSQQQSMRLANLLILISHVRHASNKGMEHLLNMKCKRVVPVYDLLLEMINAH 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLATSSRFRMMNLQ-GEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLI 182
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                                      SLTADQMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLTADOMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 60.8%; Score 759.5; DB 2; Length al Similarity 59.5%; Pred. No. 6.5e-58; 144; Conservative 56; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-530 <OGA>
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: IG7419
R;Chandrasekher, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.
R;Chandrasekher, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.
R;Chandrasekher, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.
A;Title: Progesterone receptor, but not estradiol receptor, messenger ribonucleic acid in A;Reference number: I53287; MUID:94283272; PMID:8013365
A;Accession: I67419
A;Accession: I67419
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-121 **RES>
A;Cross-references: UNIPROT:P49886; GB:S71040; NID:9547182; PIDN:AAB31102.1; PID:9547183
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;1-54/Domain: erbA transforming protein homology (fragment) <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 SSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGM 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SSTLKSLEEKDHIHRVLDKIIDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGM 120
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46.4%; Score 580.5; DB 2; Length 121;
Best Local Similarity 97.5%; Pred. No. 3.2e-43;

Matches 118; Conservative 1; Mismatches 1; Indels 1;
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Search completed: November 8, 2004, 08:28:28 Job time: 12.951 secs

218 E 218 | | | E 121

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8, 2004, 08:28:04; Search time 16.849 Seconds (without alignments) 2338.928 Million cell updates/sec
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    /cgn2 6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
    /cgn2 6/ptodata/1/pubpaa/NSO6_NEW_PUB.pep:*
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    /cgn2 6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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prodata/1/pubpaa/US10D_PUBCOMB.pep:
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*
                                                                                                                           - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                           Copyright
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 14, Appl	19,	10,	Ä	H	Sequence 2, Appli	Ä.	'n	~	ď	Sequence 13, Appl	7	61,	Sequence 128, App	55,	ď	٠,	14	7	7	9	7	42	Sequence 73, Appl	69	71,	Sequence 67, Appl	Sequence 10, Appl	16,	Sequence 8, Appli	Sequence 10, Appl	Sequence 6, Appli
US-10-157-899A-14	US-10-006-760-19	US-10-052-092-10	US-10-437-107-10	US-10-278-481-17	US-09-933-267A-2	US-09-952-680A-10	US-10-096-710-1	US-10-081-563-2	US-10-052-092-9	US-10-052-092-13	US-10-052-092-14	US-10-207-655-61	US-10-177-293-128	US-10-157-899A-55	US-10-437-107-9	US-10-437-107-13	US-10-437-107-14	US-10-095-373A-2	US-10-392-274-2	US-10-148-835-6	US-10-148-835-7	US-10-144-198-42	US-10-095-373A-73	US-10-095-373A-69	US-10-095-373A-71	US-10-095-373A-67	US-10-157-899A-10	US-10-157-899A-16	US-09-853-033-8	US-10-355-218-10	US-10-157-899A-6
14	14	14	14	14	σ	10	13	13	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	σ	15	14
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98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.3	98.2	98.0
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## ALIGNMENTS

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RESULT 1
US-10-157-899A-2
is Sequence 2, Application US/10157899A
is Publication No. US200301413559A1
is CREMEAL INFORMATION:
is Publication No. US200301413559A1
is CREMEAL INFORMATION:
is APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: Hand, Ving
APPLICANT: Kander, Gary Michael
APPLICANT: Kander, Gary Michael
APPLICANT: Kander, Gary Michael
APPLICANT: Searby, Dennis
ITILE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
ITILE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
ITILE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REPRENCE: 4-32018A
CURRENT FILING DATE: 2001-09-12
FILE REPRENCE: 2001-09-12
FILE REPRENCE: PARENTING DATE: 2001-09-12
FRIOR APLICATION NUMBER: US 60/294,839
FRIOR APLICATION NUMBER: US 60/294,839
FRIOR APLICATION NUMBER: US 60/294,839
FRIOR PAILNE DATE: 2001-09-13
FRIOR FILING DATE: 2001-09-13
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61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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Publication No. US20030207380A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
FILE REFERENCE: 2185-0648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 TLIHLMAKAGITLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1239.5; DB 9; Length 595;
Pred. No. 3.2e-118;
0; Mismatches 0; Indels 1;
                                                         GENERAL INCORNATION:

APPLICANT: CHAMBON, PIERRE
APPLICANT: CHAMBON, PIERRE
APPLICANT: METZGER, DANIELE
TITLE OF INVENTION: TRANSCENIC MOUSE FOR TARGETED RECOMBINATION
TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
FILE REPERRENCE: 065691/0222
CURRENT APPLICATION NUMBER: US/09/853,033
CURRENT FILING DATE: 2001-05-11
PRIOR PLLING DATE: 2000-10-03
NUMBER OF SEQ. DD NOS: 14
SOFTWARE: PATENTIN VET. 2.1
                   Sequence 2, Application US/09853033
Patent No. US20020100068A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6%;
Matches 244; Conservative (
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; ORGANISM: Homo sapiens
US-10-148-835-1
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CAGANISM: Homo sapiens
US-09-853-033-2
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LENGTH: 595
JS-09-853-033-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Kathryn Rene
APPLICANT: Huang, Ying
APPLICANT: Huang, Ying
APPLICANT: Kadam, Michael Joseph
APPLICANT: Kander, Gary Michael
APPLICANT: Kander, Gary Michael
APPLICANT: Zerby, Dennis
APPLICANT: Zerby, Dennis
APPLICANT: Lestrogen RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
CURRENT APPLICATION NUMBER: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/294,839
PRIOR FILING DATE: 2001-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and OTHER INFORMATION: zinc finger array(C7)
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                     120
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Pred. No. 2.1e-118;
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ence 4, Application US/10157899A
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GENERAL INFORMATION
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Local Similarity 99.6%;
hes 244; Conservative
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SOFTWARE: PatentIn version 3.1
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US-10-157-899A-4
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TYPE: PRT
ORGANISM: Homo sapiens
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                  ; ORGANISM: HC
US-10-148-835-9
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Sequence 2, Application US/10149835

JOSEPH 10 NO. US20030207380A1

RAL INFORMATION:

TITLE OF INVENTION: MUTANT ER Alpha AND TEST SYSTEMS FOR TRANSACTIVATION

FILE REFERENCE: 2185-04088F: US/10/148,835

CURRENT FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 213

SOFTWARE: PatentIn Ver. 2.0
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; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TILLE OF INVENTION:
; FILE REFERENCE: 2.105-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT PILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
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99.6%; Pred. No. 3.2e-118;
iive 0; Mismatches 0;
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Best Local Similarity 99.6
Matches 244; Conservative
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TYPE: PRT
ORGANISM: Homo mapiens
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US-10-148-835-9
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Publication No. US20030207380A1
GENERAL INFORMATION:
APPLICANT: STATO et al.
TITLE OF INVERIENCE: 2185-0648P
CURRENT APPLICANTION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SEQ ID NO 5: 220
LENGTH: 595
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     Length 595;
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       DB 14;
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Score 1239.5; DB 1.
Pred. No. 3.2e-118;
0; Mismatches 0;
  Query Match
Best Local Similarity 99.6%;
Matches 244; Conservative (
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US-10-148-835-5
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-148-835-8
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ORGANISM: Homo sapiens
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US-10-148-835-10
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Sequence 4, Application No. US20030207380A1
GENERAL INFORMATION:
GENERAL INFORMATION:
B. OF INVENTION:
CURRENT FILING DATE: 2022-10-11
SUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
ENGINE PATENTIN VER. 2.0
LENGTH: 595
US-10-148-835-3
; Sequence 3, Application US/10148835
; Publication No. US20030207380A1
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT PILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 595
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Pred. No. 1.3e-117;
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                                                                                                                                                                                                                                                                                   Query Match 98.7
Best Local Similarity 99.2
W hes 243; Conservative
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US-10-148-835-4
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Publication No. US20030207380A1
GENERAL INFORMATION:
APPLICANT: SAITO et al.
TITLE REPERBENCE: 2185-6648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 595
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US-10-148-835-8
US-10-148-835-8
Sequence 8, Application US/10148835
Publication No. US20030207380A1
FUBLICANT: SAITO et al.
TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
TITLE REFERENCE: 2185-0648P
CURRENT APPLICANTON NUMBER: US/10/148,835
CURRENT PILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SEQ ID NOS: 213
SEQ ID NO 8
LENGTH: 595
                                                                          305 SLALSLTADQWVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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98.6%; Score 1232.5; DB 14; Length 595;

Best Local Similarity 99.2%; Pred. No. 1.7e-117;

Matches 243; Conservative 0; Mismatches 1; Indels 1:
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Fri Nov 12 12:22:52

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TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
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THER INFORMATION: Homosapiens-Bacteriophage Pl
853-033-4
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APPLICANT: CHAMBON, PIERRE
APPLICANT: METZGER, DANIEL
TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
                                       Indels
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98.5%; Score 1231.5; DB 1.
ilarity 98.8%; Pred. No. 2.1e-117;
Conservative 2; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/853,033

CURRENT FILING DATE: 2001-05-11

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1

SERIOTH: 660
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ORGANISM: Artificial sequence
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|DAHRL 549
                   Similarity
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OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain OTHER INFORMATION: and a zinc finger array(C7)
                                                                APPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Kathryn Rene
APPLICANT: Huang, Ying
APPLICANT: Huang, Ying
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kadan, Michael
APPLICANT: Zerby, Dennis
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: UNPERSENCE: 4.32018A
CURRENT APPLICATION NUMBER: US/10/157,899A
PRIOR APPLICATION NUMBER: US 60/294,839
NUMBER: OF SEQ ID NOS: 55
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APPLICANT: Ge los Angeles, Joseph Ernest
APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: Huang, Ying
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kander, Gary Michael
APPLICANT: Zerby, Dennis
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
CURRENT APPLICATION NUMBER: US/10/157,899A
CURRENT FILLING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/294,839
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Pred. No. 1.7e-117;
1; Mismatches 1; Ii
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Publication No. US20030143559Al
GENERAL INFORMATION:
Sequence 8, Application US/10157899A
Publication No. US20030143559A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin version 3.1 SEQ ID NO 8
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Best Local Similarity 98.8
Matches 242; Conservative
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OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain
US-10-157-899A-14
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Publication No. US20030186385A1

GENERAL INFORMATION:

APPLICANT: Kolde, Shohei

TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF

TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF

TITLE REFERENCE: 176/60901

CURRENT APPLICATION NUMBER: US/10/006,760

RAPLICATION NUMBER: 60/249,756

RAPLICATION NUMBER: 60/249,756

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 19

LENGTH: 511
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Pred. No. 1.8e-117;
1; Mismatches 1;
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Pred. No. 2.2e-117;
0; Mismatches 1;
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
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Best Local Similarity 98.8%;
Matches 242; Conservative
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121 FDMLLATSSRFRWMNLQG-EFVCLKSIILLINSGVYTFLSSTLKSLEEKDHIHRVLDKLTD 179
                     341 FDMLLATSSRFRMMULQGEEFVCLKSIIILNSGVYTFLSSTLKSLEEKDHIHRVLDKITD
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Sequence 12, Appl
Sequence 17, Appl
Sequence 35, Appl
Sequence 2, Appli
Sequence 3, Appli
Sequence 1, Appli
Patent No. 5223606
Sequence 16, Appli
Sequence 16, Appli
Sequence 16, Appli
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Sequence 25, A
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Sequence 1, Ap
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(c) 1993 - 2004 Compugen Ltd.
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US-08-980-115-12
US-08-981-115-12
US-08-981-98-2
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FILING DATE: 13-DEC-1995
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FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: NAKAMIT INFORMATION:
REFERENCE/DOCKET NUMBER: UGAL-246/01US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE:
PRIOR APPLICATION NUMBER: GB 960550.4
FILING DATE:
APPLICATION NUMBER: GB 960550.4
FILING DATE: 15-MAR-1996
FILING DATE: 11-ARR-1996
FILING DATE: 11-ARR-1996
FILING DATE: 11-ARR-1996
FILING DATE: 08-MAY-1996
INFORMATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/EP96/03933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orphan receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08836620A Patent No. 5958710 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.2
Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 1: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                            DAHRL 244
                                                                                                                                                                                                                                                                                                                                                                       DAHRL 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: 08/764,870
ERRIER PILING DATE: 1995-12-13
ERRIER PILING DATE: 1995-12-14
ERRIER PILING DATE: 1995-12-14
ERRIER PILING DATE: 1995-12-13
EARLIER APPLICATION NUMBER: 60/008,540
ERRIER PILING DATE: 1995-12-13
EARLIER PILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
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                                                                                                                                                                                                                                                 305 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                           485 TLIHLMAKAGLTLQQQQQQQQLLLLLSHIRHMSNKGMEHLYSMKCKOVVPLYDLLLEML
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                                                                                                                                                                  Gaps
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                                                                                                                  Length 595;
                                                                                                                                                                0; Indels
                                                                                                                  DB 3;
                                                                                                                Score 1239.5; DB 3
Pred. No. 4.7e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (287)..(549)
; OTHER INFORMATION: minimal ligand binding domain US-08-980-115-12
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08980115
Patent No. 6266622
GENERAL INFORMATION:
APPLICANT: Baxter, John D.
APPLICANT: Bletterick, Robert J.
APPLICANT: Wagner, Richard L.
APPLICANT: Kushner, Peter J.
APPLICANT: Wantletti, James W.
APPLICANT: Maniletti, James W.
APPLICANT: Shiau, Andrew K.
                                                                                                                99.2%;
                                                                                                                                                              Matches 244; Conservative
                     TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-764-870-12
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                                                                                                                Query Match
Best Local Similarity
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  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-980-115-12
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120

Gaps

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61 PGFVDLTLHDQVHLLECAWLBILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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                                                                                                                                                                                                                                      METHOD FOR THE PREPARATION OF A PROTEIN
BY YEASTS USING AN INDUCIBLE SYSTEM, VECTORS AND
CORRESPONDING TRANSFORMED STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 SLALSLIADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,998
                                                                                                                                                                                                                                                                                                                                                    DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1037/98493
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                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CUSHMAN, DARBY & CUSE
STREET: 1100 NEW YORK AVE., N.W.
CITY: WASHINGTON
                                                                                                      Sequence 2, Application US/08453998; Patent No. 6444438; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION DATE: 03-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: CHAPIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 1037/
TELECHONNICATION INFORMATION:
TELECHONNE: 202-861-3711
TELECHONS: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1: Floppy disk
IBM PC compatible
                                                                                                                                                                    APPLICANT: CHAMBON, PIERRE
APPLICANT: METZGER, DANIEL
APPLICANT: WHITE, JOHN
TITLE OF INVENTION: METHOD FO
TITLE OF INVENTION: BY YEASTS
TITLE OF INVENTION: CORRESPON
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY 6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 595 amino acid
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COMPUTER READABLE FORM:
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STRANDEDNESS: siz
545 DAHRL 549
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           180 TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                    PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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                                                                                                                                                                                                                                           Sequence 135, 35 Application US/09041886

Patent No. 6235872

GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Bredesen, Sharroz
TITLE OF INVENTION: Polypeptides and Methods of Use
MHER OF SEQUENCES: 72
ORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cahryn A.
RESISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMINICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGYTH: S95 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1230.5; DB 3
Pred. No. 4.4e-124;
0; Mismatches 1;
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ilarity 99.2%;
Conservative
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COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; OLECULE TYPE: protein US-09-041-886-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 243; Conserva
                                                                                                  240 DAHRL 244
                                                                                                                                           545 DAHRL 549
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APPLICANT: Yee, Jing-Kuan
APPLICANT: Friedmann, Theodore
APPLICANT: Friedmann, Theodore
APPLICANT: Chen, Shin-Tai
TITLE OF INVENTION: Inducible Expression System
FILE REFERENCE: 6510-055CON
CURRENT APPLICATION NUMBER: US/09/566,660
CURRENT FILING DATE: 2000-05-08
PRIOR APPLICATION NUMBER: 08/693,940
PRIOR PILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATE: STEWART, Francis
TITLE OF INVENTION: REGULATION OF SITE-SPECIFIC
TITLE OF INVENTION: RECEPTOR FUSION PROTEINS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Nikaido, Marmelatein, Murray & Oram
STREET: 655 Fifteenth Street N.W. Suite 330
                                                                                                             Sequence 3, Application US/09566660 Patent No. 6432705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08564264
Patent No. 6040430
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Best Local Similarity 99.2%;
Matches 243; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: Z0005-5701
COMPUTER REALABLE FORM:
MEDIUM TYPE: Flore:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
|||||
601 DAHRL 605
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                                                                                             US-09-566-660-3
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 651
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US-08-564-264-1
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                                                                                                                               GENERAL INFORMATION:
APPLICANT: Yee, Jiing-Kuan
APPLICANT: Friedman, Theodore
APPLICANT: Chen, Shin-Tai
TITLE OF INVENTION: Inducible Expression System
TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for
TITLE OF INVENTION: Pseudotyped Retroviral Vectors
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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5e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,940
FILING DATE: 07-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 1230.5; 99.2%; Pred. No. 5e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Francis, Carol L
REGISTRATION NUMBER: 36,513
REFERNCE/DOCKET NUMBER: 6510-055001
TELECOMMINICATION INFORMATION:
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
                                                                                             Sequence 3, Application US/08693940 Patent No. 6133027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 651 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-ANG-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.2
Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LECULE TYPE: protein AGMENT TYPE: internal
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  545 DAHRL 549
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                                                          RESULT 6
US-08-693-940-3
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                                                                                                                                                                                                                                                    361 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                               1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                 Gaps
                                                                                                                                                               1;
                                                                                                      Score 1230.5; DB 4; Length 651;
Pred. No. 5e-124;
0; Mismatches 1; Indels 1;
; OTHER INFORMATION: Multi-chimeric transactivating factor US-09-566-660-3
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96.0%;
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ORGANISM: Rattus rattus
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                                                                                                                                               Best Local Similarity 98.8 Matches 242; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-836-620A-16
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                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **PIERRE; DEJEANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS, PIERRE; DEJEAN, ANNE

TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMAN, NUMBER OF SEQUENCES: 11

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (429-773)
OTHER INFORMATION: /note= "Estrogen binding domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: .misc feature
LOCATION: (1-423)
OTHER INFORMATION: /note= "FLP recombinase domain."
           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (424-428)
OTHER INFORMATION: /note= "Linker peptide.
                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02088
FILING DATE: 28-JUN-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 28-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              P564-5019
 PC-DOS/MS-DOS
                                                                                                                                                                                                                                      NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
REPERENCE/DOCKET NUMBER: PSC
TELECOMMUNICATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)638-4810
DRMATION FOR SEQ ID NO: 1:
SQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 773 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.2
Matches 243; Conservative
OPERATING SYSTEM:
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;Patent No. 5223606
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                                                                                                                                                                                                                          97.0%; Score 1213; DB 6; Length 410; 98.8%; Pred. No. 2e-122; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: 08-SEP-1995
FILING DATE: 08-SEP-1995
FILING DATE: 18-MAR-1996
FILING DATE: 15-MAR-1996
PRIOR APPLICATION NUMBER: GB 960550.4
FILING DATE: 11-ARA-1996
FILING DATE: 11-ARA-1996
FILING DATE: 08-MAY-1996
; APPLICATION NUMBER: US/07/134,130; FILING DATE: 17-DEC-1987; PRIOR APPLICATION DATA: SEQ ID NO.5: LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
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61 NGGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLINSGVYTFLSSTLKSLEEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDR
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                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
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Pred. No. 3.7e-99;
0; Mismatches 1;
                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION POR SEQ 1D NO: 10:
                                            Orphan receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08836620A
Patent No. 5958710
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                                                                                                      Floppy disk
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Best Local Similarity 99.0°
Matches 195, Conservative
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                       APPLICANT:
TITLE OF INVENTION: OTP:
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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APPLICANT:
TITLE OF INVENTION: Orph
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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    GENERAL INFORMATION:
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ORGANISM: Hom
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US-08-836-620A-9
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Patent No. 6500629

GENERAL INFORMATION:
APPLICANT: Cleaver, Brian
APPLICANT: Green, Mike L.
TITLE OF INVENTION WATERIALS and Methods for Detection and Quantitation of an Analy
FILE REFERENCE: ELI-101XC1
CURRENT APPLICATION NUMBER: US/09/660,979
CURRENT FILING DATE: 2000-09-13
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                      239
                                                                                                                                                                                                                                                                                                           490 TLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEML 549
                                                                                                                                                      370 PGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 429
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                                                                                                                     PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
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                                       SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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  4; Indels
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Pred. No. 5.1e-119;
7; Mismatches 4;
5; Mismatches
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Patent No. 5958710
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Best Local Similarity 94.7
Matches 232; Conservative
Matches 235; Conservative
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|DAHRL 554
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US-09-660-979-1
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US-08-836-620A-10
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US-09-660-979-1
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TYPE: PRT
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SEQ ID NO 1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 191; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 243;
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NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 984.5; DB 2
Pred. No. 4.4e-98;
2; Mismatches 2
APPLICATION NUMBER: PCT/EP96/03933
PILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: GB 9609576.5
FILING DATE: 10-APR-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
TYPE: Amino acids
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FILING DATE: 15-MAR-1550
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9609576.5
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APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
PTITING DATE: 15-MAR-1996
         PCT/EP96/03933
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APPLICATION NUMBER: PCT/EP96/03933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 8, Application US/08836620A
; Patent No. 5958710
; ERAL INFORMATION:
; PPLICANT:
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97.5%;
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ORGANISM: Mus musculus
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Best Local Similarity 97.5
Matches 192; Conservative
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                                                                                                                                                                                                                Length 243;
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Patent No. 6759568

GENERAL INFORMATION:
APPLICANT: YAMAGHITA, ICHIRO
TITLE OF INVENTION: High estrogen-sensitive medaka fish
FILE REFERENCE: 210217US-620-7249-0
CURRENT APPLICATION NUMBER: US/09/893,666A
CURRENT FILING DATE: 2002-02-12
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
: SEQ ID NO 2
LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                           78.4%; Score 979.5; DB 2; ilarity 97.0%; Pred. No. 1.5e-97; Conservative 2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 UVPLYDLLLEMLDAHRL 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVPLYDLLLEMLDAHRL 197
                LENGTH: 243 amino acids
TYPE: amino acids
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Oryzias latipes
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Search completed: November 8, 2004, 08:29:27 Job time : 15.4408 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
           Copyright
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sw model - protein search, using OM protein

November Run on:

8, 2004, 08:04:31; Search time 58.7592 Seconds (without alignments) 1489.639 Million cell updates/sec

US-09-830-693B-27

Perfect score: Sequence:

1 SLALSLTADOMVSALLDAEP.........CKNVVPLYDLLLEMLDAHRL 244

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 seqs, 358729299 residues sed:

2002273 number of hits satisfying chosen parameters: ľob

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

23Sep04:* geneseqp1980s:* A_Geneseq Database

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:*geneseqp2003bs:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aae35275 C7LBDAS f	Aab61498 Protein e		σ	4	Aay21626 Ligand bi	5 Human	~		Abb 76378 Human nuc	Adp05661 Human nuc		Ado42830 Human oes	Aab26784 Oestrogen	Aab26780 Human oes	Aag84509 Human oes	Ado42815 Mutant hu	Ado42820 Mutant hu	Abj15106 LBDG1 rel	Aag84507 Human oes	Ado42789 Mutant hu	Aag84508 Human oes	Aag84514 Human oes	Aag84512 Human oes	Abb76379 Cre recom
. aı	AAE35275	AAB61498	AAE35276	AAB61499	AAB36684	AAY21626	AAG84505	AAG84513	AAG84506	ABB76378	ADP05661	AD042788	AD042830	AAB26784	AAB26780	AAG84509	ADO42815	ADO42820	ABJ15106	AAG84507	AD042789	AAG84508	AAG84514	AAG84512	ABB76379
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ABP70164 AAE35278 AAE35281	ADE39222 AAU98984	ADB99352 AAY33506	AAG84511 AAG84510	AAG68251	AAU98983	AAU98988 ABB09265	ABP70163 ABB81783	ABG76090	ABK4 /448 ABU09033	AAE35283
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26 27 28		31 32	333	3 3	37	3 G 7 C	4 4 1 1	47	44	45

#### ALIGNMENTS

AAE35275 standard; protein; 414 AA

AAE35275;

(first entry) 28-MAY-2003

C7LBDAS fusion (wild-type) protein.

Oestrogen receptor; ER alpha; ligand binding domain; genetic disease; acquired disease; cell proliferative disorder; cancer; adenocarcinoma; LBD; gene switch; transgenic animal; transgenic; gene therapy; human; zinc finger array; C7; fusion protein. 

Homo sapiens. Unidentified. Chimeric.

WO200297050-A2.

05-DEC-2002.

31-MAY-2002; 2002WO-US016946.

31-MAY-2001; 2001US-0294839P

(NOVS ) NOVARTIS AG.

Ksander GM; Kadan MJ, Huang Y, De Los Angeles JE, Bracken KR, Zerby DB;

WPI; 2003-156794/15.

N-PSDB; AAD53875

New mutant estrogen receptor ligand binding domain capable of interacting with non-endogenous ligand, useful e.g. in combination with a ligand for constructing selective molecular gene switches for regulating gene

Example 4; Page 117-118; 159pp; English.

The invention relates to a mutant osstrogen receptor (ER) alpha-ligand binding domain (LBD) which comprises an amino acid modification in region 1. region 2 or both and interacting with a non-endogenous ligand as a result of the amino acid modification. Sequences of the invention are useful for treatment of genetic diseases, acquired diseases and any other conditions including cell proliferative disorders such as cancer e.g.

are useful for the preparation of therapeutic agents for treating cancer, osteoporosis and other bone disorders, Alzheimer's disease and cardiovascular diseases

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Gaps

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Length Indels

DB 4;

Score 1239.5; DB 4; Pred. No. 2.2e-124; 0; Mismatches 0;

99.2%;

Matches 244; Conservative

Similarity

Query Match Local

Sequence 422 AA;

SSSXS

120

251

191

SLALSLTADOWVSALLDAEPPILYSEYDPTRPFSEASWAGLLTNLADRELVHMINWAKRV

132

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192

121

61

252

PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVBGMVEI

1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV

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179

311

239

371

244

DAHRL

240

DAHRL 376

AAE35276 standard; protein; 438 AA.

RESULT 3 AAE35276 (first entry)

28-MAY-2003

AAE35276;

FDMLLATSSRFRMMIQGEEFVCLKSIILLNSGVYFFLSSTLKSLEEKDHIHRVLDKITD

FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD

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lung, breast, lymphoid, gastrointestinal, genito-urinary tract adenocarsionness and other malignancies such as colon cancers, renal-cell carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer of the small intestine and cancer of the oesophagus. The invention is useful for constructing selective molecular gene switches for regularing gene function in plants and transgenic animals. It is also useful in gene therapy. The present sequence is human ER alpha LBD -zinc finer array
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                                                                                                                                                                                                                          122 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                              182 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                       FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD
                                                                                                                                                                                                                                                                                                                                242 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD
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                                                                                                                                           Score 1239.5; DB 6
Pred. No. 2.1e-124;
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                                                                                                                                             sch 99.2%; sl Similarity 99.6%; 244; Conservative
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                                                                                            fusion protein
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                                                                                                                      Sequence 414 AA;
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New mutant estrogen receptor ligand binding domain capable of interacting with non-endogenous ligand, useful e.g. in combination with a ligand for constructing selective molecular gene switches for regulating gene
                                                                               Oestrogen receptor; ER alpha; ligand binding domain; genetic disease; acquired disease; cell proliferative disorder; cancer; adenocarcinoma; LBD; gene switch; transgenic animal; transgenic; gene therapy; human; zinc finger array; C7; fusion protein.
                                                                                                                                                                                                                                                                                                                   Kadan MJ, Ksander GM;
                                                                                                                                                                                                                                                                                                                   Huang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 120-122; 159pp; English
                                                        C7LBDBS fusion (wild-type) protein.
                                                                                                                                                                                                                                                                                                                    De Los Angeles JE,
                                                                                                                                                                                                                                                                     31-MAY-2001; 2001US-0294839P.
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                                                                                                                                                                                            WO200297050-A2
                                                                                                                                             Homo sapiens.
Unidentified.
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                                                                                                                                                                    Chimeric.
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Novel isoforms of human estrogen receptor alpha useful for preparing therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease and cardiovascular diseases.

LAB

(EUMO-) EURO MOLECULAR BIOLOGY

99IT-MI001433

29-JUN-1999;

27-JUN-2000; 2000WO-EP005981

WO200100823-A1

04-JAN-2001

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Flouriot

Denger S,

Gannon F,

WPI; 2001-137955/14.

The present invention relates to a human estrogen receptor (hER)-alpha isoform. Molecules which modulate the activity of the estrogen receptor

Page 45-46; 53pp; English

Claim 4;

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The invention relates to a mutant oestrogen receptor (ER) alpha-ligand binding domain (LBD) which comprises an amino acid modification in region 1, region 2 or both and interacting with a non-andogenous ligand as a result of the amino acid modification. Sequences of the invention are useful for treatment of genetic diseases, acquired diseases and any other conditions including cell proliferative disorders such as cancer e.g. lung, breast, lymphoid, gastrointestinal, genito-urinary tract adenocarcinomas and other malignancies such as colon cancers, renal-call carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer of the small intestine and cancer of the osophagus. The invention is useful for constructing selective molecular gene switches for regulating therapy. The present sequence is human ER alpha LBD -zinc finer array (C7) fusion protein
      88888888888888888888888888888888888
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Sequence 438 AA;

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PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                 FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                      TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                                                                                              TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 385
                                                                        SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                            PDMLLATSSRFRMMILQGEEFVCLKSIILLINSGVYTFLSSTLKSLEEKDHIHRVLDKITD
                                                    SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                               Gaps
                              1;
 Length 438;
                            0; Indels
  DB 6;
Score 1239.5; DB 6
Pred. No. 2.3e-124;
0; Mismatches 0;
 99.2%;
           Local Similarity 99.6
es 244; Conservative
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265

9

standard; protein; 457 AA. AAB61499 AAB61499; AAB61499 

(first entry) 54-APR-2001

Protein encoded by human estrogen receptor alpha isoform #2.

receptor alpha; cancer; osteoporosis; bone; Alzheimer's; Human; estrogen cardiovascular.

Homo sapiens

WO200100823-A1

04-JAN-2001

27-JUN-2000; 2000WO-EP005981

(EUMO-) EURO MOLECULAR BIOLOGY

99IT-MI001433

29-JUN-1999;

LAB.

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Flouriot Denger S, Gannon F,

WPI; 2001-137955/14.

Novel isoforms of human estrogen receptor alpha useful for preparing therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel two hybrid detection method comprising fusing two proteins with a DNA binding sequence and a transcription activation sequence respectively for detecting interaction of the proteins in mammalian cells.
                                                    The present invention relates to a human estrogen receptor (hER)-alpha isoform. Moleculas which modulate the activity of the estrogen receptor are useful for the preparation of theapeutic agents for treating cancer, esteoporosis and other bone disorders, Alzhaimer's disease and
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                                                                                                                                                              Score 1239.5; DB 4. Pred. No. 2.4e-124; 0; Mismatches 0;
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                         Claim 4; Page 46-48; 53pp; English.
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Best Local Similarity 99.6%;
Matches 244; Conservative
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cardiovascular diseases.
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N-PSDB; AAC88199.
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                  The present invention describes a method for detecting the interaction of a first and a second protein within a mammalian cell. The method comprises a fusion protein of the first protein with two or more transcription activation sequences (which may be the same or different), and a fusion protein of the second protein with a DNA-binding sequence. These are expressed in a mammalian cell containing DNA carrying a reporter gene downstream of a sequence binding to the DNA-binding sequence; and the expression of the reporter gene is detected to indicate interaction of the two proteins. The method is useful for the identification and examination of protein interactions within the mammalian cell, and screening of potential drugs targeting them. The present sequence represents a hybrid protein from an example given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thyroid hormone receptor; aromatic compound; ligand binding domain; alpha-glcerophosphate dehydrogenae; cardiac; obesity; triglyceride; plasma cholesterol; anti-hypertriglyceridaemic; atherosclerosis; GPDH; thyroid hormone replacement therapy; nuclear receptor.
                                                                                                                                                                                                                                                                                                                                             TLIHLMAKAGLTLOOOHORLAOLLILISHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML
                                                                                                                                                                                                                                                              SLALSLTADOMVSALLDAEPPILYSEYDPTRPPSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                  DB 4; Length 480;
                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                Score 1239.5; DB 4
Pred. No. 2.6e-124;
0; Mismatches 0;
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Shiau AK;
 Example 2; Page 35-37; 63pp; Japanese.
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West BL,
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es 244; Conser
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                                                                                                                                                       present invention
                                                                                                                                                                            Sequence 480 AA;
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                                                                                                                                         hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-gllerophosphate dehydrogenase (GPDH) levels, at levels which do not significantly modify cardiac GPDH levels and are indicated in the treatment of obesity. The compound also lower total plasma cholesterol and triglyceride levels and can be used as antipaperinglyceridaemic agents. The compound may also be used for treating atherosclerosis and may be indicated in thyroid hormone replacement therapy in patients with compounds cardiac function. Sequences AAY21621 636 amino acid sequences of ligand binding domains of several members
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                                                                                                                     The invention relates to a method for modulating activity of a thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         progesterone receptor protein; PR; pregname X receptor protein; PXR; thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR; transactivation; ERalpha; breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1239.5; DB 2;
Pred. No. 3.5e-124;
0; Mismatches 0;
Modulating activity of a thyroid hormone receptor.
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                                                               Disclosure; Fig 3G-R; 447pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the nuclear receptor superfamily
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545 DAHRL
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Sequence 595 AA;
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                                                                                                                                                                                                                                                                                                                                     The present invention relates to ligand dependent transcriptional factors including oestrogen receptor (ER) alpha and beta protein, glucocorticoid receptor protein (RR), mineralocorticoid receptor protein (RR), present activated receptor protein (RR), progretor protein (RR), present receptor protein (RR), present receptor protein (PRR), present receptor protein (PRR), present receptor protein (PRR), thyroid hormone receptor protein (PRR), thyroid hormone receptor protein (RR) and vitamin D receptor protein (VRR), the nucleic receptor protein (PRR), the nucleic gene for the ligand dependent transcriptional factor. These proteins are useful in the modulation of ligand dependent transcriptional factor. Cartivity The cells, mutant ERalpha and the polynucleotide encoding it may be used in assays for qualitatively analysing an activity for transactivation of a reporter gene by a test ERalpha, for screening transcriptional factors, for evaluating an activity for transactivation of a reporter gene by a test ERalpha and/or for presenting and recent gene by a test ERalpha and/or for presenting and recent gene by a test ERalpha and/or for presenting and recent gene by a test ERAlpha and/or for the protein screening and screen
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                                                                                                                                                                                                                                    Ligand dependent transcriptional factors, nucleic acids encoding them and cells comprising them and a specified reporter gene, useful for screening agents for the treatment of breast cancer.
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                                                                                                                                                                                                                                                                                                           Llaim 7; Page 167-170; 276pp; English
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                            21-JUL-2000; 2000JP-00220508
02-AUG-2000; 2000JP-00234053.
03-AUG-2000; 2000JP-00235460.
03-AUG-2000; 2000JP-00235461.
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Best Local Similarity 99.6
Matches 244; Conservative
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The present invention relates to ligand dependent transcriptional factors including osstrogen receptor (ER) alpha and beta protein, glucocorticoid receptor protein (RR), mineralocorticoid receptor protein (RR), progesterone protein (PR), mineralocorticoid receptor protein (PRR), receptor protein (PRR), thyroid hormone conditions them and cells comprising them and a specified reporter gene for the ligand dependent transcriptional factor. These proteins are useful in the modulation of ligand dependent transcriptional factor activity. The cells, mutant ERAlpha and the polynucleotide encoding it may be used in assays for qualitatively analysing an activity for transactivation of a reporter gene by a test ERAlpha, for screening mutant ligand dependent transcriptional factors, for evaluating an activity for transactivation of a reporter gene by a test ERAlpha and/or for screening activity for transactivation of a reporter gene by a test ERAlpha and/or for screening activity for transactivation of a reporter gene by a test ERAlpha and/or for screening activity for transactivation of a reporter gene by a test ERAlpha and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligand dependent transcriptional factors, nucleic acids encoding them and cells comprising them and a specified reporter gene, useful for screening agents for the treatment of breast cancer.
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                          glucocorticoid receptor protein; GR, mineralocorticoid receptor protein; MR; peroxisome proliferator-activated receptor protein; PPAR; progesterone receptor protein; PR; pregname X receptor protein; PXR; thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR; transactivation; ERalpha; breast cancer; mutant; mutein.
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oestrogen receptor; ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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Pred. No. 3.5e-124;
0; Mismatches 0;
dependent transcriptional factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 194-197; 276pp; English
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21-JUL-2000; 2000JP-00205080
02-AUG-2000; 2000JP-00234653.
03-AUG-2000; 2000JP-00235460.
03-AUG-2000; 2000JP-00235461.
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Best Local Similarity 99.6
Matches 244; Conservative
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Gaps

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Indels

0; Mismatches

244; Conservative

Matches

Best Local Similarity

Query Match

120

424

364

SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMGLLTNLADRELVHMINWAKRV

PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVBGMVEI FDMLLATSSRFRWMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD

61 365 121 425 180 485 240 545

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1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV

99.2%; Score 1239.5; DB 4; Length 595; 99.6%; Pred. No. 3.5e-124;

9

179

484

TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHNSNKGMEHLYSMKCKNVVPLYDLLLEML

DAHRL 244 DAHRL 549 Oestrogen; receptor; human; transgenic mouse; cytostatic; antiinflammatory; antidiabetic; endocrine; anorectic; hepatotropic.

Human nuclear oestrogen receptor alpha.

(first entry)

22-AUG-2002

ABB76378;

ABB76378 standard; protein; 595 AA

RESULT 10

ABB76378

/note= "D hinge region" 302. .552 /note= "ligand-binding domain"

28-SEP-2001; 2001WO-IB002246. 03-OCT-2000; 2000FR-00012570. 11-MAY-2001; 2001US-00853033

Claim 15; Page 170-174; 276pp; English.

WO200228175-A2

11-APR-2002

180. .262
/note= "DNA-binding domain"
263. .301

Location/Qualifiers

Homo sapiens

Domain Region Domain

TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML

239

544

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igand dependent transcriptional factors, nucleic acids encoding them and lls comprising them and a specified reporter gene, useful for screening gents for the treatment of breast cancer.
485 ILIHIMAKAGLILQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glucocorticoid receptor protein; GR; mineralocorticoid receptor protein; RR; peroxisome proliferator-activated receptor protein; PPAR; progesterone receptor protein; PR; pregname X receptor protein; PXR; thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR; transactivation; ERalpha; breast cancer; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ligand dependent transcriptional factor; oestrogen receptor; ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human oestrogen receptor alpha protein mutant K303R.
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02-AUG-2000; 2000JP-00234053
03-AUG-2000; 2000JP-00235460.
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07-JUL-2000; 2000JP-00207011
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                                                                                                                                                           DAHRL 549
                                                                                                 DAHRL 244
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                                                                                                 240
                                                                                                                                                           545
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AAG84606
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A transgenic mouse, useful in screening for medicaments for the treatment of e.g., diabetes or skin cancers, comprises a fusion protein between a recombinase Cre, and a modified ligand binding domain of the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of the human nuclear oestrogen receptor alpha (1). The invention relates to a non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ADER-) ADEREGEM ASSOC DEV RECH EN GENETIQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 131-132; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           estrogen receptor alpha.
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The present invention relates to ligand dependent transcriptional factors including oestrogen receptor (ER) alpha and beta protein, glucocorticoid receptor protein (RR), mineralecorticoid receptor protein (RR), present activated receptor protein (RR), present receptor protein (RR), present receptor protein (RR), present receptor protein (PRR), the nucleic receptor protein (PRR), the nucleic receptor protein (RR), the nucleic receptor protein (VRR), the nucleic receptor protein (RR), and vitamin D receptor protein (VRR), the nucleic receptor protein (PRR), the nucleic gene for the ligand dependent transcriptional factor. These proteins are useful in the modulation of ligand dependent transcriptional factor activity. The cells, mutant ERalpha and the polynucleotide encoding it may be used in assays for qualitativaly analysing an activity for transactivation of a reporter gene by a test ERalpha, for screening mutant ligand dependent transcriptional factors, for evaluating an activity for transactivation of a reporter gene by a test ERalpha and/or for screening a compound useful for treating a disorder of a mutant
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especially breast cancer

ERalpha,

Sequence 595 AA;

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metazoan organism, especially a transgenic mouse, characterised in that
at least one cell comprises: (i) a fusion protein formed from a
cecombinase (Creb, a hinge region (preferably human (I) D hinge), and a
cecombinase (Creb, a hinge region (preferably human (I) D hinge), and a
compliced ligand binding domain (LBD) of a nuclear osetrogen receptor,
cespecially human (I), its fragment or variant; and (ii) one or more genes
cor DNA sequences of interest belonging to the genome of the organism,
cinto which one or more recognition sites of the recombinase protein are
the cinearted. The (I) LBD domain is preferably modified by a G521R, G400V, or
combinase activity in the presence of a natural ligand such as
coetradiol, but recombinase activity is induced by a small quantity of a
synthetic ligand that has antioestrogenic activity, e.g. tamoxifen or 4-
cydroxytamoxifen. The metazoan organism or its cells, such as epidermal
cells, hepatcoytes or adipocytes, are useful in carrying out a
chinterset in its natural chromatin environment. It is also used in
certeening of medicaments for pathological conditions associated with an
calteration of the expression and/or function of the DNA sequence of
therefore the sextine and/or function of the DNA sequence of
therease, such as skin cancer, inflammation, diabetes, alopecia, obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in promoting hepatic regeneration
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Determining an increased risk for e.g. colon, brain or breast disease or disorder, by detecting a mutation or polymorphism in the nuclear receptor gene, or measuring expression or biological activity level of the nuclear

Li F; Zeng H;

JE, Gracerov A, Hohmann J, Pavlova MN, Vassilatis D,

A, Bergmann JE, Mcilwain KL, Pa

Gaitanaris GA, Madisen L,

(NURA-) NURA INC

WPI; 2004-449627/42

N-PSDB; ADP05662

receptor.

12-NOV-2003; 2003WO-US036229. 14-NOV-2002; 2002US-0426305P

Sequence 595 AA;

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305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPPSEASWMGLLTNLADRELVHMINWAKRV 364
                                                                                                                                  PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                       PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 424
                                                                                                                                                                                                                      PDMLLATSSRFRWMNLQGEEFVCLKSIILINSGVYTFLSSTLKSLEEKDHIHRVLDKITD 484
                                                                                                                                                                                                FDMLLATSSRFRMMLLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179
                                                                                                                                                                                                                                                             TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML 239
                                                                                                                                                                                                                                                                               TLIHLMAKAGLTLQQQQQQRLAQLLLILSHIRHMSNKGMEHLYSMKCKOVVVPLYDLLLEML 544
                                                                     SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                       Gaps
                                       1;
      Length 595;
                                     0; Indels
      Score 1239.5; DB 5;
Pred. No. 3.5e-124;
0; Mismatches 0;
      99.2%;
99.6%;
                                       Conservative
Query Match
Best Local Similarity
Matches 244; Conserv
                                                                                                                                                                                                                                                                                                                                                          549
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Human nuclear receptor protein SegID35 ADP05661 standard; protein; 595 AA (first entry) 26-AUG-2004 ADP05661; Ξ 

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> disease risk; disorder risk; mutation; polymorphism; muclear receptor protein; antibacterial; antithyroid; cardiovascular-Gen; cytostatic; dermatological; eating Disorders-Gen; gastrointestinal-Gen; gynaecological; hepatotropic; immunosuppressive; muscular-Gen; nephrotropic; osteopathic; virucide; adrenal gland; colon; cardiovascular; intestine; kidney; liver; lung; muscular; ovary; blood; prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus; pancreas; bone; joint; breast; immune system; metabolic; nutritive disease; human

Homo sapiens

WO2004045369-A2

03-JUN-2004

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This invention relates to a novel method of determining whether a patient has an increased risk for developing a disease or disorder which comprises determining the presence of a mutation or polymorphism in the patient of patient or in a cell of the patient. The invention may polymorphide in the patient or in a cell of the patient. The invention may be useful for the development of compounds with an antibacterial.

Co disorders-Gen, gastrointestinal-Gen, cytostatic, dermatological, eatingmunosuppressive, muscular-Gen, cytostatic, dermatological, eatingmunosuppressive, muscular-Gen, nephrotropic, osteopathic or virucide activity. The method is useful for determining whether a patient has an increased risk for developing a disease or disorder. The nucleic acid cencoding a nuclear receptor polypeptide, an expression vector comprising the nucleic acid operably linked to a promoter, or a compound that cencoding a nuclear setup for treating or preventing a disease or disorder of the adrenal gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular, covary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid, uterus, pancreas, bone and joints, breast, or immune system, or metabolic or nutritive disease or disorder. The present sequence is that of a nuclear receptor protein which may be used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 35; 508pp; English.
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Best Local Similarity 99.6
Matches 244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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ADO42788 standard; protein; 595 AA. RESULT 12 ADO42788 ID ADO4

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New mutant estrogen receptor-alpha useful for determining effectiveness of treatment by estrogen receptor activity regulator substance and
                                                                      human; oestrogen receptor-alpha; ER; ER activity regulator substance; anti-oestrogen substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 19; 111pp; Japanese.
                                              Human oestrogen receptor-alpha
                                                                                                                                                                                                                                                  15-NOV-2002; 2002JP-00331994.
15-NOV-2002; 2002JP-00331995.
15-NOV-2002; 2002JP-00331996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 199.2%;
Local Similarity 99.6%;
Les 244; Conservative C
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              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 595 AA;
                                                                                                                                                         WO2004046352-A1.
                                                                                                                             Homo sapiens
              26-AUG-2004
                                                                                                                                                                                        03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                    Fujimori K;
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                                                                                                   human; oestrogen receptor-alpha; ER; ER activity regulator substance; anti-oestrogen substance.
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                                                                             Wild type human oestrogen receptor-alpha (ER) protein
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Pred. No. 3.5e-124;
0; Mismatches 0;
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15-NOV-2002; 2002JP-00331995.
15-NOV-2002; 2002JP-00331996.
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Best Local Similarity 99.6
Matches 244; Conservative
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                                                                                                                                                                                          WO2004046352-A1
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The invention comprises the amino acid sequences of mutant human oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the invention are useful for determining the effectiveness of a treatment by an ER activity regulator substance, and for determining the effectiveness of a treatment by an anti-oestrogen substance. The present amino acid sequence represents a human ER protein.
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                                                                                                                                                                                                                                                              Length 595;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                        Score 1239.5; DB 8;
Pred. No. 3.5e-124;
0; Mismatches 0;
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RESULT 13 ADO42830

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Homology model; ligand binding domain; glucocorticoid receptor; AIDS; hypertension; diabetes; obesity; glaucoma; depression; wound; protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.
      Oestrogen receptor protein sequence.
                                                                       01-MAR-2000; 2000WO-GB000727.
                                                                                  99GB-00004441.
99GB-00009151.
                                                                                                            Greenidge P;
                                                                                                  KARO-) KARO BIO AB.
                                                                                                                       WPI; 2000-549565/50.
                                                 WO200052050-A2
                                      Unidentified
                                                                                  01-MAR-1999;
                                                                                       22-APR-1999;
                                                            08-SEP-2000,
                                                                                                             illner M,
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Designing a homology model of the ligand binding domain of a glucocorticoid receptor displayed as a three-dimensional image, useful for identifying agonists and antagonists for treating e.g. inflammation, hypertension, glaucoma, diabetes.

Disclosure; Fig 6; 246pp; English.

This invention relates to a method for designing an homology model of the ligand binding domain of a glucocorticoid receptor. The homology model may be displayed as a three-dimensional image. The method comprises: (a) providing an amino acid sequence and an x-ray crystallographic structure to take of the ligand binding domain of a thyroid, oestrogen or progesterone creeptor; (b) modifying the x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domain of the glucocorticoid receptor and the thyroid, oestrogen, or progesterone receptor; (c) verifying the accuracy of the homology confided by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying confided by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying confidence of ligands for the glucocorticoid receptor; and designing ligands confidence of inflammation and also in immunosuppressive therapy. The identified agonists are useful for the treatment of hypertension, diabetes, and wounds the homology models are also useful for electronic screening of compound datebases, de novo drug design and/or prediction of binding confinities of glucocorticoid receptor models produced using molecular mechanics scoring functions. The prediction of the correction contains produced using co-ordinate data for the glucocorticoid receptor models produced using coestrogen and progesterone receptors. The present sequence repetore of the method of the invention for homology modelling of a glucocorticoid creceptor for the coestrogen and progesterone receptors. The present sequence repetored using method of the invention for homology modelling of a glucocorticoid creceptor for the glucocorticoid receptors are sections. The present sequence repetored using method of the invention for homology model is useful for the glucocorticoid receptor for the glucocor

Sequence 244 AA;

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61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                           PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                     SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                       Gaps
                                       1;
     Length 244;
                                     0; Indels
DB 3;
98.8%; Score 1235.5; DB 3 99.6%; Pred. No. 2.8e-124; ive 0; Mismatches 0;
                 Best Local Similarity 99.6
Matches 243; Conservative
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240 Designing a homology model of the ligand binding domain of a glucocorticoid receptor displayed as a three-dimensional image, useful for identifying agonists and antagonists for treating e.g. inflammation, Homology model; ligand binding domain; glucocorticoid receptor; AIDS; hypertension; diabetes; obesity; glaucoma; depression; wound; human; protein co-ordinate data; thyroid hormone receptor; oestrogen receptor. 121 FDWLLATSSRFRMWALQGBBFVCLKSIILLNSGVYTFLSSTLKSLBEKDHIHRVLDKITD 181 TLIHLMAKAGLTLQQQQQQRLALILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEML Human oestrogen receptor protein sequence. AAB26780 standard; protein; 244 AA. 99GB-00009151. 01-MAR-2000; 2000WO-GB000727. 99GB-00004441 18-JAN-2001 (first entry) Greenidge (KARO-) KARO BIO AB. WPI; 2000-549565/50. 240 DAHR 243 DAHR 244 01-MAR-1999; Homo sapiens. 22-APR-1999; 08-SEP-2000. Gillner M, AAB26780; 121 180 241 RESULT 15 AAB26780 a g ð ò 유

This invention relates to a method for designing an homology model of the ligand binding domain of a glucocorticoid receptor. The homology model may be displayed as a three-dimensional image. The method comprises: (a) providing an amino acid sequence and an x-ray crystallographic structure for the ligand binding domain of a thyroid, oestrogen or progesterone ceeptor; (b) modifying the x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domain of the glucocorticoid receptor and the thyroid, oestrogen, or progesterone receptor; (c) verifying the accuracy of the homology comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying the homology model for greater consistency with the binding properties. The homology model for greater consistency with the binding properties. The homology model is useful for drug screening and designing ligands (agonists and antagonists) acrossing to a glucocorticoid receptor. The identified agonists are useful for the treatment of inflammation and also in immunosuppressive therapy. The identified account of the treatment of antagonists are useful for the treatment of antagonists are useful for the treatment of bypertension, diabetes, observed. and wounds. The homology models are also useful for electronic screening of compound databases, de novo drug design and/or prediction of binding affinities of glucocorticoid receptor ligands for the receptor by

Disclosure; Fig 2A; 246pp; English. hypertension, glaucoma, diabetes.

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molecular mechanics scoring functions. The specification contains protein co-ordinate data for the glucocorticoid receptor models produced using the method, based on the X-ray crystallographic structure of the cestrogen and progesterone receptors. The present sequence represents the human oestrogen receptor protein. The protein is used in an example of the method of the invention for homology modelling based on the thyroid
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Sequence 244 AA;

Gaps 1; Score 1235.5; DB 3; Length 244; Pred. No. 2.8e-124; 0; Mismatches 0; Indels 1; 0; Indels Query Match
Best Local Similarity 99.6%;
Matches 243; Conservative

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FDMLLATSSRFRMMNLQG-EFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITD 179 121

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TLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMBHLYSMKCKNVVPLYDLLLEML 239 180

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DAHR 244

Search completed: November 8, 2004, 08:26:23 Job time : 60.7592 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 8, 2004, 08:05:27 ; Search time 45.1837 Seconds (without alignments) 3132.595 Million cell updates/sec Run on:

US-09-830-693B-28 1230 1 SLALSLTADQMVSALLDAEP......CKNVVPLYDLLLEMLDAHRL 246 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 number of hits satisfying chosen parameters: 1825181 segs, 575374646 residues Searched: To

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	P03372 homo sapien	Q6qis5 bos taurus	Aas46251 bos tauru	P19785 mus musculu	P06211 rattus norv	Q29040 sus scrofa		_	Q9tv98 equus cabal	Q91250 poephila gu	P06212 gallus gall	Q765n7 alligator m	Bad08348 alligator	Q8ayh0 coturnix co	Q8cgk8 cavia porce	Q95113 ovis aries		Q9yht3 anolis caro	Q6w5g5 xenopus lae	Aag84784 xenopus l	Q6w5g9 xenopus tro	Aag84780 xenopus t	Q6w5g7 xenopus lae	Aag84782 xenopus l	P81559 xenopus lae	Q6w5g6 xenopus lae	Aaq84783 xenopus l	Q91424 cnemidophor			Q800q2 zoarces viv
ID	ESR1_HUMAN	060155	AAS46251	ESR1 MOUSE	ESR1_RAT	ESR1_PIG	ESR1_MESAU	QBUWBO	ESR1_HORSE	ESR1 POEGU	ESR1_CHICK	Q765 <u>N</u> 7	BAD08348	Q8AYH0	Q8CGK8	Q95L13	Q8UWA9	ESR1 ANOCA	Q6W5 <u>G</u> 5	AAQ84784	Q6W5G9	AAQ84780	Q6W5G7	AAQ84782	ESR1_XENLA	Q6W5G6	AAQ84783	ESR1 CNEUN	Q902 <u>E</u> 6	ESR1 BOVIN	Q800 <u>Q</u> 2
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Length	595	296	296	599	9	595	595	587	594	587	589	587	587	589	353	431	581	349	427	427	543	543	585	585	286	427	427	307	542	174	570
* Query Match	98.1	92.6	92.6	95.2	94.9	94.7	94.3	93.2		93.0	93.0	92.9	92.9	95.6	92.5	92.5	90.3	89.7	84.8	84.8	84.8	84.8	84.8	84.8	84.3	84.0	84.0	80.7	67.5	67.4	0.99
Score	1206.5		1175.5	1171.5	1167.5	1164.5	1159.5	1146.5	4	1144.5	1143.5	1142.5	1142.5	1139.5	1137.5	1137.5	1110.5	1103.5	1042.5	1042.5		1042.5	1042.5	1042.5	1037.5	1033.5	1033.5	992.5	~	828.5	811.5
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808.5 808.5 806.5 799.5 794.5 794.5	789 789 786 785.5
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 1 5 6 4 6

# ALIGNMENTS

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WEDLINE-95140025; PubMed=7838153;
Arnold S.P., Obourn J.D., Jaffe H., Notides A.C.;
"Serine 167 is the major estradiol-induced phosphorylation site on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20565767; PubMed-11113208; DOI=10.1128/MCB.21.1.343-353.2001; Sauve F., McBroom L.D.B., Gallant J., Moraitis A.N., Labrie F., Giguere V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coactivator essential for ligand-dependent transactivation by nuclear
         Pfeffer U., Fecarotta E., Castagnetta L., Vidali G.,
"Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-
responsive human breast cancer cell lines.";
Cancer Res. 53:741-743(1993).
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                                                                                                                                                                                                                                                                                                                         MEDLINE=95280953; PubMed=7539106;
Arnold S.F., Obourn J.D., Jaffe H., Notides A.C.;
"Phosphorylation of the human estrogen receptor on tyrosine 537 in
vivo and by src family tyrosine kinases in vitro.";
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"Solution structure of the DNA-binding domain of the oestrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION SITES SER-104 AND SER-106, AND MUTAGENESIS.
                                                                                                                                                                                                                   human breast carcinoma.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                           SEQUENCE OF 110-117, PHOSPHORYLATION, AND MUTAGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sar receptor interacting determinant."; Cell. Biol. 21:343-353(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 274:34283-34293(1999).
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MEDLINE=93153765; PubMed=7916651;
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                                                                                                                                                                              TISSUE-Breast carcinoma;
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INTERACTION WITH NCOAG.
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Anderson T.1., Wooster R., Laake K., Collins N., Warren W., Skrede M., Ralderson T.1., Wooster R., Laake K., Dowsett M., Olsen A.O., Beles R., Tveit K.M., Johnston S.R.D., Dowsett M., Olsen A.O., Moeller P., Stratton M.R., Boerresen-Dale A.-L.;

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-! FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in Larget tissues.

-!- SUBDNIT: Binds DNA as a homodimer. Binds UBEIC (By similarity).

Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 306-544.
MEDLINE-98262297; PubMed=9600906;
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Agard D.A., Greene G.L.;
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J. Biol. Chem. 267:9868-9873(1992)
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MEDLINE=98280806; PubMed=9619507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 389:753-758(1997).
                                                                                                                                                                                    Cell 75:567-578(1993).
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03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Batrogen receptor alpha.
Bos taurus (Bovine).
Bos taurus (Rovine).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bovinae; Bos
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Nishimura N., Tetsuka M.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS18775; AAS46251.1; -.
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ESR1 MOUSE
1D ESR1 MOUSE STANDARD; PF
AC P19765; Q9JUT5; Q9QY51; Q9QY52;
DT 01-FEB-1991 (Rel. 17, Created)
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Matches 229; Conservative
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NCOA6 coactivators, leading to a strong increase of transcription of target genes.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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                                                             Query Match 98.1%; Score 1206.5; DB 1; Length Best Local Similarity 96.3%; Pred. No. 1.8e-109; Matches 237; Conservative 0; Mismatches 8; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Estrogen receptor alpha.
Bos taurus (Bovine).
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RA SEQUENCE FROM N.A.

RA ACAINE-C37BL/6J; TISSUB-Bone, and Thymus; RA FEDLINE-2234683; PubMed=12466851; DOI=10.1038/nature01266; RA FEASH Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Akaido I., Osato N., Saito R., Nogami A., Schombach C., Golobori T., Adachi J., Bono H., Kondo S., RA Agai K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Golobori T., Radarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Balda E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gasaferland T., Gariboddi M., Gissi C., Godzik A., Gough J., RA Garai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Maltani H., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Magoshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., RA Ravashi T., Need J.C., Reed D.J., Raing B.L., Miki H., RA Ravashi T., Red J.C., Reed D.J., Raing B.L., Ring B.L., Marchionni L., McKenzie L., Miki H., RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Schneider C., Semple C.A., Setou M., Shimada K., Verardo R., Wajner L., Wahlestedt C., Wang Y., Watenabe Y., Wall R., Yang L.G., Wynshaw-Boris A., Yanagisawa M., Sarazume N., Saro K., RA Hirzane-Kishikawa T., Konno H., Nakamura M., Saro K., RA Hara A., Hashizume W., Innetani K., Ishii Y., Itoh M., Kagawa I., Rayazaki A., Yashine, Y., Sasaki D., Shinagawa A., Toth M., Waterston R., Asakai Y., Rayani I., Rayazaki A., Sakai V., Sasaki D., Shinagawa A., Toth M., Waterston R., Asakaini Y., Itoh M., Wargers J., Aizawa A., Hashizume W., Innetani Y., Itoh M., Waterston R., Rayawa I., Rayazaki A., Yashinaki Y., Sasaki D., Shibata K., Shinagawa A., Itoh M., Waterston R., Lander E.S., Rogers J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiang M.S., Hart G.W.; "A subpopulation of estrogen receptors are modified by O-linked N- \,
                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]
SEQUENCE OF 269-599 FROM N.A.
SEQUENCE OF 269-599 FROM N.A.
STRAIN-SJL/J, and BIO.S/J; TISSUE-Spleen;
Ma R.Z., Teuscher C.;
"Screening for candidate genes of mouse autoimmune diseases.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                            MEDLINE=91042558; PubMed=2484714;
White R., Lees J.A., Needham M., Ham J., Parker M.;
"Structural organization and expression of the mouse estrogen
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name=Esrl; Synonyms=Nr3al, ESR, Estr, Estra;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE-LINKAGE SITES SER-10; THR-50 AND SER-575
MEDLINE=21124487; PubMed=11226831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. Chem. 272:2421-2428(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYDRATE-LINKAGE SITE SER-575.
MEDLINE=97153020; Pubmed=8999954;
                                                                                                                                                                                                                                                                                                                                      Endocrinol. 1:735-744 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-22 FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,770 full-length cDNAs.";
ture 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 477:15-20(2000)
                                                                                         musculus (Mouse).
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                            TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                   receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESR2. Interacts with NCOA3 and NCOA6 coactivators, leading to a strong increase of transcription of target genes. Interacts with NCOA5. Binds UBEIC (By similarity).

-!- SUBCELUIAR LOCATION; Nuclear.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
-!- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).
-!- MISCELLANBOUS: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R EMBL; A410621, GRAFEZSB111; -.

R HSSP; P03372; 1HCP.

R TRANSFAC; T00259; -.

GlycoSuiteDB; P19768; -.

R GO; GO:0016628; C:chromatin remodeling complex; ISS.

R GO; GO:0016629; C:chromatin remodeling complex; ISS.

R GO; GO:0016020; C:membrane; ISB.

R GO; GO:0030234; C:mcleus; IDA.

R GO; GO:0030235; F:nitric-coxide synthase regulator activity; ISS.

R GO; GO:0030235; F:nitric-coxide synthase regulator activity; ISS.

R GO; GO:003025; P:nitric-coxide synthase regulator activity; ISS.

R GO; GO:003025; P:negaling receptor activity; ISS.

R GO; GO:0006355; P:negaling receptor signaling pathway; ISS.

R GO; GO:0006355; P:negaling of transcription, DNA-dependent; ISS.

R InterPro; IPR001229; Osetrgn_receptor.

R InterPro; IPR00123; Stdhrmn_receptor.

R InterPro; IPR001346; Str_ncl_receptor.
                                                                         INTERACTION WITH NCOA3.
MEDLINE=97336097; PubMed=9192892;
Torchia J., Rose D.W., Inostroza J., Kamei Y., Westin S., Glass C.K.,
Rosenfeld M.G.;
                                                                                                                                                                                                                                                                                                                                                    peroxisome proliferator-activated
                                                                                                                                                                                                                                                                                      MEDLINE=20250907; PubMed=10788465;
Zhu Y.-J., Kan L., Qi C., Kanwar Y.S., Yeldandi A.V., Rao M.S.,
                                                                                                                                                                                                                                                                                                                                                                             receptor (PPAR) interacting protein (PRIP) as a coactivator for
                                                                                                                                                                  "The transcriptional co-activator p/CIP binds CBP and mediates nuclear-receptor function.";
Nature 387:677-684(1997).
Cheng X., Hart G.W.; "Glycosylation of the murine estrogen receptor-alpha."; J. Steroid Biochem. Mol. Biol. 75:147-158(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                      Chem. 275:13510-13516(2000).
                                                                                                                                                                                                                                                                                                                                                      "Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, M38651; AAA37580.1; -.
EMBL, AK036627; BAC29510.1; -.
EMBL, AK041525; BAC3093.1; -.
EMBL, AJ276597, CAB85618.1; -.
EMBL, AF128221; AAF22562.1; -.
EMBL, AF128220; AAF22561.1; -.
                                                                                                                                                                                                                                                                  INTERACTION WITH NCOA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subfamily
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SEQUENCE FROM N.A.
   309 SPALSLTADQMVSALLDAEPPMIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV 368
                                                                                                                                                                                                                                                                                                                                                                                                                       PGFGDLMLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVGGWVEI 428
                                                                                                                                                                                                                                                                                                                                                                                                           61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FDMLLATSSRFRAMNLQGEBFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEM 547
                                                                                                                                                                                                                                                                                                                                                                      1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
                           Pfam; PF00105; zr-cw, r. PRINTS; PR00643; OBSTROCENR.
PRINTS; PR00047; STRDHORMORR.
PRINTS; PR00047; STRDHORMORR.
PRINTS; PR00047; STROIDFINGER.
PRINTS; PR00047; STROIDFINGER.
SWART; SM00430; HOLL; 1.
SWART; SM00430; LOLL; 1.
SWART; SW00339; Zr C4; 1.
SWART; SW00339; Zr C4; 1.
DNA-binding; Glycoprotein; Nuclear protein; Phosphorylation; Receptor; Steroid-binding; Transcription regulation; Zinc-finger.

Modulating.
                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).

Eukaryota; Metazos (Rat).

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
                                                                                                                                                                                           Phosphoserine (by CDK2) (By similarity)
Phosphoserine (by CDK2) (By similarity)
Phosphoserine (By similarity).
Phosphoserine (by (K2) (By similarity).
Phosphotyrosine (by Tyr-kinases) (By
                                                                                                                                                                                                                                                                                                                                DB 1; Length 599;
                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                           similarity)
O-linked (GlCNAC).
O-linked (GLCNAC).
//FIGA-CAR (OOLS).
E - O (in strain SJL/J).
L - M (in Ref. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Last sequence update)
01-07-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name=Esrl; Synonyms=Nr3a1, Esr; Estr;
                                                                                                                                                                                                                                                                                                              OSFSE2FC21CC0A8B CRC64;
                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.9e-106, 5; Mismatches 11;
                                                                                                                                                                         Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 AA
                                                                                                                                                                                                                                                                                                                               95.2%; Score 1171.5; 93.1%; Pred. No. 4.96
                                                                                                                                                                                    Poly-Ala.
                                                                                                                                             C4-type.
C4-type.
                                                                                                                                                                Hinge.
  InterPro; IPR001628; Znf_C4steroid
        Pfam; PF00104; Hormone recep; 1. Pfam; PF02159; Oest_recep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
                                                                                                                                                                                                                                                                                                              66955 MW;
                                                                                                                                                                                                                                                                                                                                                 Matches 229; Conservative
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50
575
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269
599 AA;
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                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                  DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
DOMAIN
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CARBOHYD
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MOD RES
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MOD RES
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1 target tissues.

1 target tissues.

2 -1- SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ERR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes (By similarity). Binds UBBIC.

2 -1- SUBCELLULAR LOCATION: Nuclear.

3 -1- SUBCELLULAR LOCATION: Nuclear.

3 -1- DOWAIN: Composed of three domains: a modulating N-terminal domain.

3 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

3 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

4 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

5 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

5 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

5 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

5 -1- PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

5 -1- STMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fan M., Long X., Bailey J.A., Reed C.A., Osborne E., Gize E.A., Kixk E.A., Bigby R.W., Nephew K.P.;

"Ithe activating enzyme of NBDDB inhibits steroid receptor function.";

Mol. Endocrinol. 16:315-330(2002).

-i- FUNCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation
                                                                                                                                                                                                                                         Koike S., Sakai M.;
"Molecular cloning and characterization of rat estrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley; TISSUE=Uterus;
Maggi A.M.A.;
Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
                                                                         Submitted (MAR-1987) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO, GO:0016049; P:cell growth, ISS.
GO, GO:0045839; P:negative regulation of mitosis; ISS.
InterPro; IPR000536; Hrmon_recept_lig.
InterPro; IPR001292; Oestron_receptor.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR001628; Ztdr.ncl_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; Hormone_recep; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 15:2499-2513 (1987).
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PRINTS; PRO0398; STRDHORNONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=87174780; PubMed=3031601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X0102; CAA68287.1; -. EMBL; X61098; CAA43411.1; -. PIR; S07379; QRRTE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [4]
INTERACTION WITH UBELC.
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TRANSFAC; T00258; -.
RGD; 2581; E8r1.
                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=11818503;
STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily.
                                      Muramatsu M.
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30S SPVLSLTADQMISALLEAEPPIIYSEYDPTRPLSEASMMGLLTNLADRELVHMINWAKRV 364
to a strong increase of transcription of target genes. Binds UBEIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE, PS00031; NUCLEAR RECEPTOR; 1.
Direct protein sequencing; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
OEC23DC3085BF001 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear receptor-type.
C4-type.
C4-type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00543; OESTROGENR.
PRINTS; PR00394; STRDHORNONER.
PRINTS; PR00047; STROLDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinge.
                      SUBCELLULAR LOCATION: Nuclear
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                                                                                                                                                                                                                                                      EMBL; Z37167; CAA85524.1; -. PIR; I47140; I47140.
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250
2250
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70
104
1106
1118
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SMART; SM00399; ZNF C
PROSITE; PS00031; NUCI
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185
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221
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64
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ZN FING
ZN FING
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Matches
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                                                                                                                                                                                                                                                                                            310 SPALSLTADQMVSALLDAEPPLIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV 369
                                                                                                                                                                                                                                                                                                                           PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                                                                                                                                                                                                  429
                                                                                                                                                                                                                                                                                                                                                                         121 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXEEKDHIHRVLDKIT 180
                                                                                                                                                                                                                                                                                                                                                                                             430 FDMLLATSSRFRAMNLQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIN 488
                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                489 DTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEM 548
                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell. Endocrinol. 104:163-172(1994).

VENCTION: Nuclear hormone receptor. The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues (By similarity).

SUBNUIT: Binds DNA as a homodimer. Can form a heterodimer with BSR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading
                                                                                                                                                                                                                                                                                1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                370 PGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                                                                                                     DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                                                                                                                                                                                                                         Gaps
                                                                                                                            (By similarity)
(By similarity)
                                                                                                                                                   similarity).
CK2) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Uterus;
MEDLINE=95080454; PubMed=7988744;
Boekenkamp D., Jungblut P.W., Thole H.H.;
Inthe C-terminal half of the porcine estradiol receptor contains no post-translational modification: determination of the primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                        1;
                                                                                                                                                Phosphoserine (By similarity).
Phosphoserine (by CK2) (By simila:
Phosphotyrosine (by Tyr-kinases)
                                                                                                                                                                                                                                  DB 1; Length 600;
                                                                                                                                                                                                                                                        12; Indels
PROSITE, PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Phosphorylation; Receptor;
Steroid-binding; Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
                                                                                                                                                                                                            C9C7D8CACE0F57D8 CRC64;
                                                                                                                            (by CDK2)
(by CDK2)
                                                Nuclear receptor-type.
                                                                                                                                                                                                                                 Score 1167.5; DB 1
Pred. No. 1.2e-105;
                                                                                                                                                                                                 (in Ref. 3)
                                                                                          Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 595 AA.
                                                                                                                            Phosphoserine
Phosphoserine
                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                     similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                     Modulating
                                                                                                        Poly-Ala.
                                                                    C4-type.
                                                                                                                  Poly-Ser
                                                                               Hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=ESR1; Synonyms=NR3A1, ESR;
Sus scrofa (Pig).
                                                                                                                                                                                                            67030 MW;
                                                                                                                                                                                                                                 94.9%;
                                                                                                                                                                                                                                                        228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDAHRL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDAHRL 554
                                                                                                                                                                                                            600 AA;
                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                       1190
226
226
316
64
171
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9040;
                                             DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                            SEQUENCE
                                                                                                      DOMAIN
DOMAIN
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                 CONFLICT
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MOD_RES
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                                                                                           DOMAIN
                                     DOMAIN
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ESR1_PIG
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DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

PTM: Phosphorylated by cyclin A/CDK2 (By similarity).

MISCELLANEOUS: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R HISSP, P03372; IHCD.

R GO; GO:0016585; C:chromatin remodeling complex; ISS.

GO; GO:0016585; C:chromatin remodeling complex; ISS.

R GO; GO:0030284; F:cetrogen receptor activity; ISS.

R GO; GO:0030285; F:nitric-oxide synthase regulator activity; ISS.

R GO; GO:0030525; F:nitric-oxide synthase regulator activity; ISS.

R GO; GO:0030520; P:cell growth; ISS.

R GO; GO:0045839; P:cell growth; ISS.

R GO; GO:0045839; P:negative regulation of mitosis; ISS.

R GO; GO:006355; P:regulation of transcription, DNA-dependent; ISS.

R InterPro; IPR001292; Oestrgn receptor.

InterPro; IPR001292; Oestrgn receptor.

InterPro; IPR001628; Std. Armon-receptor.

InterPro; IPR001628; Std. C4steroid.

R Ffam; PF0014; Hormone_recept.

R Pfam; PF0014; Hormone_recept.

R Pfam; PF00152; C4f-G1:1.

R Pfam; PF00152; C4f-G1:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphoserine (by CDK2) (By similarity). Phosphoserine (by CDK2) (By similarity).
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Phosphoserine (by CK2) (By similarity).
Phosphotyrosine (by Tyr-kinases) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXEKDHIHRVLDKIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPALSLTADQMVSALLDAEPPLIYSEYDPSRPPSEASMMGLLTNLADRELVHMINWAKRV
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R GO; GO:0016049; P:cell growth; ISS.
GO; GO:0016049; P:cell growth; ISS.
R GO; GO:00045839; P:negative regulation of mitosls; ISS.
R GO; GO:0006355; P:regulation of transcription, DNA-dependent; ISS.
R InterPro; IPR001292; P:regulation of transcription, DNA-dependent; ISS.
R InterPro; IPR001293; HTMON recept 1ig.
R InterPro; IPR001293; Stdimm, receptor.
R InterPro; IPR00146; Str_ncl_receptor.
R InterPro; IPR001628; Znf_C4steroid.
R Pfam; PF02159; Oset_recep; 1.
R Pfam; PF02159; Oset_recep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphoserine (by CDK2) (By similarity). Phosphoserine (by CDK2) (By similarity).
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Phosphoserine (by CK2) (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%; Score 1159.5; DB 1; Length 595; ilarity 91.5%; Pred. No. 7.3e-105; Conservative 8; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBITION OF THE PROBLEM OF THE PROB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear receptor-type
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinge.
Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly-Pro.
Poly-Ser.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-type.
C4-type.
                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0543; OESTROGENR.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; Znf_C4steroid; 1.
SMART; SM00430; ADLI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66833 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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198
290
595 AA;
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Matches 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DNA BIND
ZN_FING
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SEQUENCE
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MOD_RES
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MOD_RES
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                                                  DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
                                                                                                                                                                                                                                                            (By similarity).

SUBCELLUIAR LOCATION: Nuclear.

DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                             PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                             PDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 98-291 FROM N.A. Jubbers L.S., Petersen S.L., Wade G.N.; "Return of lordosis after food deprivation and refeeding in Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
Mesocricetus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           imster estrogen receptor cDNA: cloning and mRNA expression.";
Steroid Biochem. Mol. Biol. 72:47-53(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Estradiol receptor) (ER-alpha).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRI_MESAU STANDARD; PRT; 595 AA.
1090245; 0902066;
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2004 (Rel. 45, Last annotation update)
01-CCT-2004 (Rel. 45, Last annotation update)
Name=ESR1; Synonyma=NR3A1, ESR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Uterus;
MEDLINE=20197937; PubMed=10731637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF181077; AAD53956.1; -. EMBL; AF184276; AAF02721.1; -. HSSP; P03372; 1HCQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhat H.K., Vadgama J.V.;
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LDAHRL 549
                                                                                                                                                                                                                                                                                                                                 LDAHRL 246
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EMBL; AF124093; AAD17316.1; -.
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2245
3310
70
104
1106
1118
536
                                                                                 NCBI_TaxID=9796;
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221
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ZN FING
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299 SPALSLTAEQWYSALLEAEPPIVYSEYDPNRPENEASMMTLLTNLADRELVHMINWAKRV 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                SEQUENCE FROM N.A.
MEDLINE=21490797; PubMed=11604222;
Sumida K., Ooe N., Saito K., Kaneko H.;
"Molecular cloning and characterization of reptilian estrogen receptor
                                                                                                                                                                                                                                    R GO; GO:0016585; C:chromatin remodeling complex; ISS.
R GO; GO:0016585; C:chromatin remodeling complex; ISS.
R GO; GO:00103020; C:membrane; ISS.
R GO; GO:0030235; F:nitric-coeptor activity; ISS.
R GO; GO:003025; F:nitric-coeptor activity; ISS.
R GO; GO:000355; F:nitric-coeptor signaling pathway; ISS.
R GO; GO:000035; Humon receptor signaling pathway; ISS.
R InterPro; IPR001292; Oestrgn receptor.
R InterPro; IPR001292; Oestrgn receptor.
R InterPro; IPR001294; Std. Tol. receptor.
R InterPro; IPR001628; Znf_C4sTeroid.
R Pfam; PF00129; Oest recep; 1.
R Pfam; PF00129; Oest recep; 1.
R Pfam; PF00105; Zf-C4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
             Estrogen receptor.
Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Crocodylidae, Alligatorinae, Caiman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                 MOI. Ceil. Endocrinol. 183:33-39(2001).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SUBLELLULAR LOCATION: Nuclear (By similarity).
EMBL; AB055220; BAB79436.1; -- HSSP; P03372; 1HCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 93.2%; Score 1146.5; DB 2; Length Best Local Similarity 90.7%; Pred. No. 1.3e-103; Matches 223; Conservative 11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SW00430; HOLL; 1.
SWART; SW00399; ZnF C4; 1.
SMORT; SW00399; ZnF C4; 1.
DROSITE; PS000031; NUCLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription regulation; Zinc; Zinc-finger.
SROUENCE 587 AA; 66513 MW; DB17F2B837FCF513 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 AA
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(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00543; OESTROGENR.
PRINTS; PR001398; STRDHORNONER.
PRINTS; PR00047; STROIDPINGER.
PRODOM; PD000035; Znf_C48teroid; 1.
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                                                                     NCBI_TaxID=8499;
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ESR1 HORSE
ID ESR1 HORSE
AC Q9TV98,
DT 16-OCT-2001 (
DT 16-OCT-2001 (
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Mol. Cell
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Best Local S
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M SEQUENCE FROM N.A.

M MCDOWell K.J., Adams M.H., Green M.L., Cleaver B.D., Sharp D.C.;

M MCDOWell K.J., Adams M.H., Green M.L., Cleaver B.D., Sharp D.C.;

L Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

L Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

Teceptors are involved in the regulation of eukaryotic gene repression and affect cellular proliferation and differentiation in target tissues (By similarity).

C SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ESR2. Interacts with NCOA3, NCOA5 and NCOA6 coactivators, leading to a strong increase of transcription of target genes.Binds UBBLC (By similarity).

C -- SUBCELLULAR LOCATION: Nuclear.

C -- SUBCELLULAR LOCATION: Nuclear.

C -- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.

C -- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphoserine (by CDK2) (By similarity). Phosphoserine (by CDK2) (By similarity). Phosphoserine (By similarity). Phosphoserine (by CK2) (By similarity). Phosphotyrosine (by Tyr-kinases) (By similarity).
                                                                                                         Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
01-OCT-2004 (Rel. 45, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha)
Name-ESR1; Synonyme-NR3A1, ESR;
Equue caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating.
Nuclear receptor-type.
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SPAISLTAEOMVSALLEAEPPLVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRV 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The chicken oestrogen receptor sequence: homology with v-erbA and human oestrogen and glucocorticoid receptors.";
                                  DNA-dependent; ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
BEDILINE-86247578; PubMed=3755102;
Krust A., Green S., Argos P., Kumar V., Walter P., Bornert J.-M.,
Chambon P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 587;
     GO:0030520; P:estrogen receptor signaling pathway; ISS: GO:0006355; P:regulation of transcription, DNA-depender
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               SMARY; SM00399; ZDF C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Steroid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
Name=ESR1; Synonyms=NRJA1, ESR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2B254168A7A910AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nuclear receptor-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.0%; Score 1144.5; DB 30.2%; Pred. No. 2.1e-103 iive 12; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating.
                                                      InterPro; IPR000536; Hrmon recept lighterPro; IPR01292; Oestrgn_receptor. InterPro; IPR001723; Stdhrmn_receptor. InterPro; IPR008946; Str nol receptor. InterPro; IPR008946; Str nol receptor. InterPro; IPR00898; Znf C46Feroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; Zinc-finger
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PRINTS, PRO0398; STRDHORMONER.
PRINTS, PRO0047; STROIDFINGER.
PRODOM; PD000035; Znf C48teroid;
SMART; SM00430; HOLL: 1.
                                                                                                                                                                                          Pfam; PF00104; Hormone_recep; 1. Pfam; PF02159; Oest_recep; 1. Pfam; PF00105; zf-C4; 1.
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Best Local Similarity 90.2'
Matches 222; Conservative
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587 AA;
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                                                                                                                                                                                             PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                           FDMLLATSSRFRMMILQGBEFVCLKSIILLNSGVYTFXXXXXXXXEEKDHIHRVLDKIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            542
                                                                                                                                                                1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain. SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97163508; PubMed=9010328; MEDLINE=97163508; PubMed=9010328; MEDLINE=97163508; PubMed=9010328; MEDLINE=97163508; PubMed=9010328; Arnold A.P., Campagnoni A.T.; Zebra finch estrogen receptor cDNA: cloning and mRNA expression."; Steroid Biochem. Mol. Biol. 59:135-145(1996).

- FUNCTION: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

-- SUBGNIT: Binds DNA as a homodimer. Can form a heterodimer with ER beta (By similarity).

-- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poephila guttata (Zebra finch) (Taeniopygia guttata).
Wkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae; Passeriformes; Estrildidae,
Estrildinae; Taeniopyja.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0016585; C:chromatin remodeling complex; ISS.
GO:0016020; C:membrane; ISS.
GO:0030284; F:estrogen receptor activity; ISS.
GO:0030284; F:estrogen receptor activity; ISS.
                                                                                                                5
                                                            Length 594;
                                                                                                             12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2004 (Rel. 44, Last annotation update)
Estrogen receptor (ER) (Estradiol receptor) (ER-alpha).
DD36CA7C24C74B95 CRC64;
                                                   Score 1146; DB 1;
Pred. No. 1.5e-103;
                                  93.2%; bcc. No. 191.5%; Pred. No. 191.5%; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             587 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
  66103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L79911; AAB81108.1; -. HSSP; P03372; 1HCP.
                                                                                                       Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
594 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDAHRL 246
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                                                                                Similarity
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NCBI_TaxID=59729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subfamily.
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SEQUENCE
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                                                      Query Match
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                                                                                   Best Local
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RESULT 10 ESR1 POEGU

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Gaps

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121 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXXEEKDHIHRVLDKIT 180
299 SPALSLTAEQMVSALLEAEPPIVYSEYDPNRPFNEASMMTLLTNLADRELVHMINWAKRV
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                                                                                                       DILIHLMAKAGLILQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                                                                                                                                     DTLIHLMAKSGLSLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S.,
Actsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S.,
Actsu Y., Remudez D.S., Bryan T.A., Guillette L.J., Iguchi T.;
"Wolecular cloning of the estrogen and progesterone receptors of the
T. "Molecular cloning of the estrogen and progesterone receptors of the
T. "SUBCELLIAR LOCATION: Nuclear (By similarity).

I. SUBCELLIAR LOCATION: Nuclear (By similarity).

I. SIMILARITY: Belongs to the nuclear hormone receptor family.

EMBL; AB118909; BAD08448.1; -.

EMBL; AB118909; BAD08448.1; -.

InterPro; IPR001292; Oestrgn receptor.

InterPro; IPR001292; Oestrgn receptor.

InterPro; IPR0018946; Str nol, receptor.

IN Pfam; PF00118; 26-04; 1.

IN Pfam; PF00118; 26-04; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alligator mississippiensis (American alligator).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Alligator.
NCBI_TaxID=8496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tch 92.9%; Score 1142.5; DB 2 al Similarity 90.2%; Pred. No. 3.3e-103; 222; Conservative 12; Mismatches 11;
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PRINTS; PRO0398; STRODDENGER.
PRINTS; PRO0047; STROIDFINGER.
ProDom; PD000035; Znf_C4steroid; 1.
SMART; SM00430; HOL!; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 27, (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Estrogen receptor a.
                                                                                                                                                                                                                                          LDAHRL 246
                                                                                                                                                                                                                                                                                                        538 LDAHRL 543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=ERa;
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Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstands.

The European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way offitied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 418
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D J. 5:891-897 (1986). FUNCTION: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. SUBUNIT: Binds DNA as a homodimer. Can form a heterodimer with ER-
                                                                                                                                                                                         -!-SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: Composed of three domains: a modulating N-terminal domain, a DNA-binding domain and a C-terminal steroid-binding domain.
-!- MINGELLANEOUS: In the absence of ligand, steroid-binding domain.
-!- AINCELLANEOUS in the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO: GO:0016585; C:chromatin remodeling complex; ISS.

R GO: GO:0016585; C:chromatin remodeling complex; ISS.

R GO:0010284; F:estrogen receptor activity; ISS.

R GO: GO:0030235; F:nitric-oxide synthase regulator activity; ISS.

R GO: GO:003025; F:nitric-oxide synthase regulator activity; ISS.

R GO: GO:003025; F:nitric-oxide synthase regulator activity; ISS.

R GO: GO:000635; P:regulation of transcription, DNA-dependent; ISS.

R InterPro; IPR00129; Oestrgn receptor.

R InterPro; IPR00129; Oestrgn receptor.

R InterPro; IPR00146; Str incl receptor.

R InterPro; IPR001628; Znf C48teroid.

R Pfan; PF0014; Hornone_recep; 1.

R Pfan; PF0015; Zef-Gf; I.
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ART; SM00399; ZNF C4; 1.

OSITE; PS00031; NUCLEAR RECEPTOR; 1.

ONA-binding; Nuclear protein; Receptor; Steroid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steroid-binding.
1B092233C770A54B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating
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C4-type.
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PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PRO00035; EAT C48teroid; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X03805; CAA27433.1; -. PIR; A40914; QRCHE. HSSP; PO372; 1HCP. TRANSPAC; T00264; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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245
305
589 AA;
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ZN FING
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Local Similarity .-
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 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PDMLLATSSRFRMMLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLIHLMAKSGLSLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEM 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
          DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                                                                                                                                                                                                                                                                                                                                                 1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Estrogen receptor alpha.
Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                    Alligator mississippiensis (American alligator).
Jkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Alligator.
                                                                                                                                                                                                                                                  Katsu Y., Bermudez D.S., Braun E.L., Helbing C., Miyagawa S., anderson M.P., Kohno S., Bryan T.A., Guillette L.J., Iguchi T., "Molecular cloning of the estrogen and progesterone receptors of American alligator."
                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                          Length 587;
                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                       587 AA; 66497 MW; FC217FCC0F1B41F0 CRC64;
                                                                                                                             14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          92.9%; Score 1142.5; DB 2; 90.2%; Pred. No. 3.3e-103;
                                                                                                                                                                                                                                                                                                                                                              12; Mismatches
                                                                                                             Ş
                                                                                                            587
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                                                                                                                                                                                                                                                                                               Gen. Comp. Endocrinoi. 150:122.
EMBL; AB115909; BAD08348.1; -.
                                                                                                                                                                                                                                                                                                                                                            Matches 222; Conservative
                                                                                                           PRELIMINARY;
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                                       LDAHRL 246
                                                          LDAHRL 543
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                                                                                                                                                                                                                                                                                                                                                    Similarity.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coturnix.
NCBI_TaxID=93934;
                                                                                                                                                                                                                                        TISSUE=Gonad
                                                                                                                             14-APR-2004
14-APR-2004
                                                                                                                                                                                                                                                                                          Comp.
                                                          538
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                  478
                                       241
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BAD08348;
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                                                                                                                                                                              R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005496; F:steroid binding; IEA.

R GO; GO:0003707; F:steroid hormone receptor activity; IEA.

R GO; GO:0003700; F:regulation factor activity; IEA.

R GO; GO:0003700; F:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR001292; Oestrgn_receptor.

R InterPro; IPR001292; Std.mol_receptor.

R InterPro; IPR001465; Str.nol_receptor.

R Pfam; PF00104; Hormone_recept; 1.

R Pfam; PF00104; Hormone_recept; 1.

R Pfam; PF00105; zf-G4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FDMLLATSSRFRMMNLQGEEFVÇLKSIILLNSGVYTFXXXXXXXXXEKDHIHRVLDKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
Ichikawa K., Yamamoto I., Tsukada A., Saito N., Shimada K.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-- SUBCELLULAR LOCATION: Nuclear (By similarity).

-- SUBLARITY: Belongs to the nuclear hormone receptor family. EMBL; AF442965; AAN63674.1; -- HSSP; P03372; 1HCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0543; OESTROGENR.
PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0036; STRDHORMONER.
ProDom: PD000035; Znf_C4steroid; 1.
SMART; SM00399; Znf_C4; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 589 AA; 66767 MW; 8271FDAA67552CA4 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.8%; Pred. No. 6.6e-103; tive 12; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92.6%; Score 1139.5;
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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63 SPALSLTADQWVSALMDAEPPILYSEYDAVKPPSEASMMGLITNLADRELVHMINWAKRV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 DTLIHLMAKAGLTLQQQHRRLAQLLLISHIRHMSNKGVEHLYNMKCKNVVPLYNLLLEM 301
            Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLUTAR LOCATION: Nuclear (By similarity).

-!- SUBCELLUTAR LOCATION: Nuclear (By similarity).

EMBL; AXIV2106; AAN86120.1; -.

GO; GO:0003634; C:nucleus; IEA.

GO; GO:0003707; F:stearoid hormone receptor activity; IEA.

GO; GO:0003707; F:stearoid hormone receptor activity; IEA.

GO; GO:0003707; F:transcription of transcription, DNA-dependent; IEA.

R GO; GO:0003707; F:transcription of transcription, DNA-dependent; IEA.

R InterPro; IPR00355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR00356; Str_nol_receptor.

R InterPro; IPR00456; Str_nol_receptor.

R InterPro; IPR00456; Str_nol_receptor.

R PFGM; PF001104; Hormone receptor.

R Pfam; PF001104; Hormone receptor.

R PRINTS; PR00430; ACT (3.1.

R PRINTS; PR00430; HOLI; 1.

M PTANSCRIPTION regulation; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                  92.5%; Score 1137.5; DB 2; Length 89.4%; Pred. No. 5.7e-103; ive 12; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                            VON TER 1 1 1 1 2 20 ENCE 353 AA; 40099 MW; C298827350700510 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Matcn
Best Local Similarity 89.4$
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDAHRL 246
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302 LEAHRL 307
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le : 46.1837 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein

November Run on:

8, 2004, 08:14:27; Search time 12.049 Seconds (without alignments) 1964.426 Million cell updates/sec

US-09-830-693B-28 1230 1 SLALSLTADQMVSALLDAEP.......CKNVVPLYDLLLEMLDAHRL 246 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues

Searched:

283416 number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ø	Description	estrogen receptor	estroden receptor		ч	80K estrogen recep	estrogen receptor			c	estrogen receptor		estrogen receptor		estrogen receptor	_	steroid hormone re	estrogen receptor	steroid hormone re	glucocorticoid rec	progesterone recep		progesterone recep			progesterone recep	retinoid receptor	retinoid X recepto	glucocorticoid rec	retinoid X recepto
SUMMARIÉS					_	_	٠		_		_	•	_	••	••	•		_			_			_			_		_	•
SU	9	QRHUE	QRMSE	ORRTE	I47140	S64737	ORCHE	ORXLE	T10423	858224	S71400	JC5939	A37197	JW0046	\$26595	167419	B29345	S58087	A29345	S60586	A25923	QRHUP	A39596	153280	A43781	A35466	C41977	150515	A54273	809592
	DB	П	ч	7	~	~	-	-	~	~	~	7	~	~	~	~	~	~	~	~	~	Н	7	~	N	~	~	~	7	П
	Length	595	599	900	595	701	589	286	620	535	477	530	574	503	133	121	433	433	521	758	930	933	923	923	467	786	488	441	771	462
dir	Ouery Match	97.4	95.2	94.9	94.7	93.1	93.0	84.3	64.4	63.5	62.2	62.2	61.7	61.0	50.9	44.5	30.4	œ	26.3	21.4	20.5	20.5	20.1	20.0	19.8	19.8	19.6	19.5	19.4	19.2
	Score	1197.5	1171.5	1167.5	1164.5	•	1143.5		792.5	781.5	764.5	764.5	758.5	750.5	626.5	547.5	374.5	354.5	323	263.5	248	248	247	246	243.5	243	241.5	240		236.5
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retinoic acid rece	retinoid X recepto	retinoic acid rece	retinoid-X recepto	retinoid receptor	glucocorticoid rec	glucocorticoid rec	glucocorticoid rec	retinoid X recepto	androgen receptor	retinoid X recepto	retinoic acid rece	H-2 region II bind	retinoid X recepto	retinoic acid rece	RXR-betal isoform
S26668	A47278	S26670	B41727	D41977	QRHUGA	A25691	QRHUGB	150514	JG0194	S37781	S26669	A34418	D41727	A41651	184718
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467 2	467 2	463 2	463 2	470 2	777 1	783 1	742 1	379 2	848 2	533 2	410 2	446 2	448 2	451 2	520
		19.1 463 2													
19.2		19.1	19.1	19.0	18.7	18.7		18.5	18.3	18.1	18.0	18.0		18.0	18.0

### ALIGNMENTS

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RESULT 1
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estrogen receptor 1 - human

NiAlternate names: ERI; estrogen receptor alpha
C;Species: Homo sapiens (man)
C;Species: Gila; Homo sapiens (man)
C;Species: Gila; Homo sapiens (man)
B;Species: Gila; Homo sapiens (man)
B;Species: Man, Homo sapiens (man, Homo sapiens (man)
B;Species: Man, Homo sapiens (man)
B;Species: Man, Homo sapiens (man, Homo sapiens (man,

A;Molecule type: mRNA A;Reaidues 1.595 cGR1. A;Cross.references: UNIRROT:Q14268; UNIFROT:Q9UB35; GB:M12674; NID:g182192; PIDN:AAA5239 R;Green, S.; Walter, P.; Kumar, V.; Krust, A.; Bornert, J.M.; Argos, P.; Chambon, P. Rature 320, 114-1139, 1386 A;Title: Human oestrogen receptor CDNA: sequence, expression and homology to v-erb-A. A;Reference number: A931376; MUID:86146892; PMID:3754034

A; Accession: A93376

A;Molecule type: mRNA A;Residues: 1-595 <GR2>

A;Cross-references: GB:X03635; NID:g31233; PIDN:CAA27284.1; PID:g31234 R;Ponglikitmongkol, M.; Green, S.; Chambon, P. EMBO J. 7, 3385-3388, 1988 A;Fitle: Genomic organization of the human oestrogen receptor gene. A;Fitle: Genomic organization of the human oestrogen receptor gene. A;Feference number: A43021; MUID:89091079; PMID:3145193

A;Accession: A43021 A;Molecule type: DNA A;Residues: 143-161,205-225;244-264;356-374,'G',376;402-422;447-460,'P',462-467;508-528 R;Kesveney, M.; Klug, J.; Gamnon, F. DNA Seq. 2, 347-358, 1992 A;Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene A;Reference number: S27140; WUID:93075998; PMID:1476547

A; Accession: S27143

A;Status: preliminary; translation not shown A;Molecule type: DNA Residues: 1-115 <KEA>

A;Cross-references: EMBL:X62462, NID:g31201; PIDN:CAA44122.1; PID:g31205
R;Pfeffer, U.; Fecarotta, E.; Castagnetta, L.; Vidali, G.
Cancer Ness 53, 741-743, 1993
A;Title: Estrogen receptor variant messenger RNA lacking exon 4 in estrogen-responsive him. A;Reference number: S34000; MUID:93153765; PMID:7916651

A;Status: preliminary ;Accession: S34000

A; Molecule type: mRNA

A)Residues: 216-254,367-399,'G',401-434 <PFE>
A)Cross-references: EMBL:X73067; NID:g579865; PIDN:CAA51528.1; PID:g939886
A)Note: the authors translated the codon GGG for residue 400 as Val
R;Dots, H.; Alkhalaf, M.; Murphy, L.C.
Mol. Endocrinol. 6, 773-785, 1992
A)Title: Characterization of estrogen receptor variant mRNAs from human breast cancers.

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Query Match
Best Local Similarity 93.1%;
Matches 229; Conservative
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A; Accession: S16731
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A; Reference number: A41925; MUID:92293154; PMID:1603086
A; Accession: A41925
A; Molecule type: mRNA
A; Residues: 1-214' ELPTLC' <DOT>
A; Cross-references: GB:M69297; NID:g182218; PIDN:AAA58462.1; PID:g182219
A; Experimental source: clone 4; breast cancer
A; Note: sequence has been revised after extraction from NCBI backbone
A; Note: sequence extracted from NCBI backbone (NCBIN:106580)
A; Mote: sequence extracted from NCBI backbone (NCBIN:106580)
A; Status: significant sequence differences
A; Molecule type: mRNA
A; Cross-references: GB:M69296
A; Experimental source: clone 24; breast cancer
A; Note: sequence extracted from NCBI backbone (NCBIN:106597)
C; Comment: The steroid hormones and their receptors are involved in the regulation of complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
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Pred. No. 5.36
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95.9%;
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C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly ¢ omplex appears to recognize discrete DNA sequences upstream of transcriptional start site C;Superfamily: estrogen receptor; erA transforming protein homology
C;Superfamily: estrogen receptor; erA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept F;1-183/Domain: amino-terminal kNHI2>
F;184-275/Domain: amino-terminal kNHI2>
F;187-460/Domain: erA transforming protein homology kERBA>
F;187-460/Domain: erA transforming protein homology kERBA>
F;187-460/Domain: ainc finger CCCC motif F;23-245/Region: zinc finger CCCC motif F;23-245/Region: zinc finger CCCC motif F;23-245/Region: sire finger CCCC motif F;23-245/Region: sire finger CCC motif F;23-245/Region: steroid binding #stetus predicted cSTB>
F;189-192-266,209/Rinding site: zinc (Cys) #status predicted
F;240,309/Binding site: zinc (Cys) #status predicted
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A,Residues: 1-487, 'T',489-600 <MAG>
A,Rolecule type: mRNA
A,Residues: 1-487, 'T',489-600 <MAG>
A,Residues: 1-487, 'T',489-600 <MAG>
A,Residues: 1-487, 'T',489-600 <MAG>
A,Cross-references: EMBL.Xx61098, NID:956120, PIDN:CAA43411.1; PID:956121
A,Cross-references: EMBL.Xx61098, NID:956120, provinced in the regulation of eul C;Comment: The steroid hormones and their receptors are thought to be weakly somplex appears to recognize discrete DNA sequences upstream of transcriptional start site omplex appears to recognize discrete DNA sequences upstream of transcriptional start site.
C;Superfamily: estrogen receptor; erbA transforming protein homology created hormone recept F;1-184/Domain: amino-terminal xMIZ>
F;188-461/Domain: DNA binding #status predicted <DNA>
F;188-461/Domain: erbA transforming protein homology <ERBA>
F;188-461/Domain: arine finger CCCC motif F;242-424(Asegion: zinc finger CCCC motif F;261-276(Region: nuclear location signal F;305-557/Domain: steroid binding #status predicted <STB>
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Nucleic Acids Res. 15, 2499-2513, 1987

A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.

A;Reference number: S07379; MUID:87174780; PMID:3031601

A;Accession: S07379

A;Molecule type: mRNA

A;Kesidues: 1-600 <KOI.

A;Kesidues: 1-600 <KOI.

A;Kesidues: 1-600 <KOI.

B;Maggi, A.M.A.

Submitted to the EMBL Data Library, June 1991
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Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Accession: S07379; S16731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 SPALSLTADQMVSALLDAEPPMIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV
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Pred. No. 2.1e-108;
5; Mismatches 11; Indels
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A;Residues: 1-701 <PIN>
A;Cross-references: EMBL:U47678; NID:g1197854; PIDN:AAB00115.1; PID:g1197855
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ripink, J.J.; Wu, S.Q.; Wolf, D.M.; Bilimoria, M.M.; Jordan, V.C.
Nucleic Acids Res. 24, 962-969, 1996
A; Title: A novel 80 kDa human estrogen receptor containing a duplication of exons A; Reference number: S64737; MUID:96174665; PMID:8600466
A; Recession: S64737
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: estrogen receptor; erbA transforming protein homology C;Reywords: steroid hormons receptor; zinc finger F:183-456/Domain: erbA transforming protein homology 
F;181-456/Domain: erbA transforming protein homology #status atypical <F:518-562/Domain: erbA transforming protein homology #status</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                 181 DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                                                                                                                                                                                                                                                                                                                                  484 DTLIHLMAKAGLTLQQQHRRLAQLLLILSHFRHMSNKGMEHLYNMKCKNVVPLYDLLLEM
                                                                                                                                                                            PGFVDLTLHDQVHLLECAWLE1LM1GLVWRSMEHPGKLLFAPNLLLDRNOGKCVEGMVE1
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                 Length 595;
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                                                     Indels
            DB 2;
                                                 12;
          Score 1164.5; DE
Pred. No. 1e-107;
7; Mismatches 1
                                                   7;
        Query Match
Best Local Similarity 91.9%;
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80K estrogen receptor - human
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C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 12.Feb-1997 #sequence revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: 147140; S66250; $32402
R;Bokenkamp, D.; Jungblut, P.W.; Thole, H.H.
Mol. Cell. Endocrinol. 104, 163-172, 1994
A;Title: The C-reminal half of the pordine estradiol receptor contains no post-translat
A;Reference number: 147140; MUID:95080454; PMID:798874
A;Reference number: 147140
A;Reference trype: mRNA
A;Residues: 1-595 &BOK>
A;Cross-references: UNIPROT:Q29040; EMBL:Z37167; NID:9587554; PIDN:CAA85524.1; PID:95875
A;Evr. J. Biochem. 231, 510-516, 1995
A;Cross-references: uterus
R;Thole, H.H.; Maschler, I.; Jungblut, P.W.
Eur. J. Biochem. 231, 510-516, 1995
A;Cross-references: number: S66250; MUID:95361877; PMID:7635163
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F,190,193,207,210/Binding site: zinc (Cys) #status predicted F;226,232,242,245/Binding site: zinc (Cys) #status predicted F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted
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A. e: Surface mapping of the ligand-filled C-terminal half of the ligand-compact of the ligand-filled C-terminal half of the ligand-compact of the ligand-filled C-terminal half of the lighter number: 866250, MUID:95361877; PMID:7635163

A. Accession: 866250

A. Molecule type: protein
A. Residues: 297-307;310-313;320-323;337-340;417-420;466-473

R. R. Experimental source: uterus

R. Thole, H. H.
                                                                                                                                 1;
                                                                                        DB 1; Length 600;
                                                                                      Score 1167.5; DB 1; Length
Pred. No. 5.2e-108;
5; Mismatches 12; Indels
                                                                                   Query Match
Best Local Similarity 92.7%;
Matches 228; Conservative
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LDAHRL 554
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605 QQHQRLAQLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRL 655

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FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
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80.1%; Pred. No. 4.3e-95;
iive 25; Mismatches 23; Indels
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A, Experimental source: strain d-rR, liver
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A;Molecule type: mRNA
A;Residues: 1-620 <OKA>
A;Cross-references: UNIPROT:P50241; EM
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Matches 197; Conservative
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C;Comment: The steroid hormones and their receptors are involved in the regulation of eu C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly omplex appears to recognize discrete DNA sequences upstream of transcriptional start sit C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recept; F;11-173/Domain: DNA binding #status predicted <DNA>
F;177-265/Domain: amino-terminal <NH2>
F;177-260/Domain: and finger CCCC motif
F;250-265/Region: zinc finger CCCC motif
F;250-265/Region: storid binding #status predicted <STB>
F;284-366/Domain: steroid binding #status predicted (STB>
F;281-3123/Binding site: zinc (Cys) #status predicted F;252,21231,234/Binding site: zinc (Cys) #status predicted F;212-225/Binding site: zinc (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: UNIPROT: P06212
R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
EMBO J. S., 891-897, 1986
A; The Chicken oestrogen receptor sequence: homology with v-erbA and the human oes
A; Cence number: S07192; MUID: 86247578; PMID: 3755102
                                                                                           estrogen receptor - chicken
Cispecies: Gallus gallus (chicken)
Cjate: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
CjAccession: A40914; 807192
R;Maxwell, B.L.; McDonnell, D.P.; Conneely, O.M.; Schulz, T.Z.; Greene, G.L.; O'Malley,
Mol. Endocrinol. 1, 25-35, 1987
A;Title: Structural organization and regulation of the chicken estrogen receptor.
A;Reference number: A40914; MUID:88318621; PMID:2901032
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Peb-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40907
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                                                                                                                                                                                                                                                                                               A; Status: not compared with conceptual translation
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A;Residues: 1-256,'E',258-589 <KRU>
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Best Local Similarity 90.21
Matches 222; Conservative
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A; Residues: 1-589 < MAX>
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transcription regulation
C;Species: Oryzias sp.
A;Variety: strain d-rR
A;Variety: strain d-rR
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T10423
R;Okada, H:; Kawahara, T:; Yamashita, I.
submitted to the RMBL Data Library, March 1994
A;Description: Cloning of medaka estrogen receptor cDNA.
A;Reference number: Z17013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: estrogen receptor; erbA transforming protein homology C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcripF;184-460/Domain: erbA transforming protein homology <ERB>
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R;Mosselman, S.; Polman, J.; Dijkema, R.
ENSS Lett. 392, 49-53, 1996
A;Title: ER-beta: identification and characterization of a novel human estrogen receptor
A;Reference number: S71400; MUID:96354875; PMID:8769313
                                                                                                                    Afforced type: mRNA
A;Residues: 1-477 <MOS.
A;Residues: 1-477 <MOS.
A;Cross-references: EMBL:X99101; NID:g1518262; PIDN:CAA67555.1; PID:g1518263
A;Cross-references: EMBL:X99101; NID:g1518262; PIDN:CAA67555.1; PID:g1518263
C;Superfamily: estrogen receptor; erbA transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep:
F;94-355/Domain: erbA transforming protein homology <ERBA>
F;94-355/Domain: ainc finger CCCC motif
F;132-156/Region: zinc finger CCCC motif
F;132-156/Region: nuclear location signal
F;52/Binding site: phosphate (Ser) (covalent) (by MAP kinase) #status predicted
F;96,99;113,116/Binding site: zinc (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000
C; Accession: JC5939
R; Ogawa, S.; Inoue, S.; Watanabe, T.; Hiroi, H.; Orimo, A.; Hosoi, T.; Ouchi, Y.; Muramat Biochem. Biophys. Res. Commun. 243, 122-126, 1998
A; Title: The complete primary structure of human estrogen receptor beta (hERbeta) and its A; Reference number: JC5939; MUID:98139878; PMID:9473491
A; Accession: JC5939
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-530 cogga>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNOGKCVEGMVEIFDM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKITDTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 IHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       385 VWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVVVVDLLLEMLNA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:AB006590; NID:g2911151; PIDN:BAA24953.1; PID:g2911152 C;Superfamily: estrogen receptor; erbA transforming protein homology F;147-408/Domain: erbA transforming protein homology <ERB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 SLTADOMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                            62.2%; Score 764.5; DB 2; 59.3%; Pred. No. 4.8e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.2%; Score 764.5; DB 2; Best Local Similarity 59.3%; Pred. No. 5.5e-68; Matches 144; Conservative 52; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 59.3%; pred. No. 4.8e-
Matches 144; Conservative 52; Mismatches
                                                                                                     A; Accession: S71400
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                                                                                                 65 DLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDML 124
                                                                                                                                                                                      LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDH----IHRVLDKIT 180
                                                                                                                                                                                                                                                                                     DTLIHLMAKAGLTLQQQHQRLAQLLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM. 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 QELSLHDQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRSEGDCVEGMAEIFDM 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNOGKCVBGMVEIFDM 123
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                                                                         5 SLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFV 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oestrogen receptor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S5824
R;Rogers, S.A.; Llewellyn, L.; Ramsurn, V.P.; Sweeney, G.E.; Wigham, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                estrogen receptor beta - human
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Jun-2000
C;Accession: S71400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGF
                                 Gaps
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A.Accession: $5824
A.Accession: $5824
A.Accession: $5824
A.Accession: $5824
A.Molecule type: mRNA
A.Residues: 1-535 <ROG>
A.Cross-references: UNIPROT: P50242; EMBL:X89959; NID: 9929901; PIDN: CJ
C.Superfamily: estrogen receptor; erbA transforming protein homology
C.Keywords: steroid hormone receptor; zinc finger
F;103-382/Domain: erbA transforming protein homology <RBBA>
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                                 43; Indels
           Pred. No. 1.1e-70;
63.0%; Preα. νω.
Five 39; Mismatches
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                              Conservative
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       Similarity
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    Best Local
Matches 15
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Matches 15
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A,Title: A novel isoform of rat estrogen receptor beta with 18 amino acid insertion in the A, Reference number: JW0046, MUID:98262932; PMID:9600083
A, Accession: JW0046
A, A, Accession: JW0046
A, Residues: 1-503 < AMAR>
A, Residues: 1-503 < AMAR>
A, Residues: 1-503 < AMAR>
Cross-references: DDBJ:AB012721
C, Comment: This protein functions as a negative regulator of estrogen action.
C, Superfamily: estrogen receptor; erbA transforming protein homology
F;102-381/Domain: erbA transforming protein homology < ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Groupen receptor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Decies: Bos primigenius taurus (cattle)
C;Decies: Bos primigenius taurus (cattle)
C;Decession: $26595
R;Hagen-Mann, K.; Mann, W.; Meyer, H.H.D.
Submitted to the EMBL Data Library, May 1992
A;Reference number: $26595
A;Reference number: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----RNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXX 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 ATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKITDTLIH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 LTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LALSLTADOMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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                                                                                                                                                                                                                                                                                                                                                                                                                     44; Indels
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                                                                                                                                                                                                                                                                                                                                               61.0%; Score 750.5; DB 2;
55.3%; Pred. No. 1.3e-66;
ive 51; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 50.9%; Score 626.5; DB 2 al Similarity 92.5%; Pred. No. 5.4e-55; 124; Conservative 0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         estradiol receptor - rhesus macaque (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 YSMKCKNVVPLYDLLLEMLDAHRL 246
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                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 55.3
nes 146; Conservative
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 124
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A, Residues: 150-574 < PA2>
A, Residues: 150-574 < PA2>
A, Cross-references: GB: M31559; NID: g213783; PIDN: AAA49552.1; PID: g213784
C, Superfamily: estrogen receptor; erbA transforming protein homology
C, Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; 2i
F, 145-421/Domain: erbA transforming protein homology < ERBA>
F, 146-421/Domain: erbA transforming protein homology < ERBA>
F, 140-167/Region: zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Pakdel, F.; Le Guellec, C.; Vaillant, C.; Le Roux, M.G.; Valotaire, Y.
Mol. Endocrinol. 3, 44-51, 1989
A;Title: Identification and estrogen induction of two estrogen receptors (ER) messenger
A;Reference number: A40070; MUID:89127284; PMID:2915648
A;Accession: A40070
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rainbow trout estrogen receptor
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NyAlternate names: Exbeta2
C;Species: Rattus norvegicus (Norway rat)
C;Dete: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 17-Mar-1999
C;Accession: JW0046
R;Marryyana, K.; Endoh, H.; Sasaki-Iwaoka, H.; Kanou, H.; Shimaya, E.; Hashimoto, S.;
Biochem. Biophys. Res. Commun. 246, 142-147, 1998
                                                                            437
                                                                                                                                               279 EQVLFLLQGQTPALCSRQKVARPYTEVTMMTLLTSMADKELVHMIAWAKKVPGFQELSLH 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 DQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRSEGDCVEGMAEIFDMLLATVS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 RFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKITDTLIHLMAK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXEEKDHIHRVLDKITDTL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    estrogen receptor - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
R;Dels: 31-Jan-1992 #sequence revision 31-Jan-1992 #text_change 20-Aug-1999
C;Accession: F; Le Gac, F; Le Goff, P; Valotaire, Y.
Model: Endocrinol. 71, 195-204, 1990
A;Reference number: A37197, MUD:91006824; PMID:2210031
A;Reference number: A37197
A;Status: preliminary
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                                                    380 LLATTSRFRELKLOHKEYLCVKAMILLNSSMYPLVTATQDADSSRK--LAHLLNAVTDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 QMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 758.5; DB 2;
; Pred. No. 2.4e-67;
35; Mismatches 54;
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Best Local Similarity 62.09
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: mRNA
A,Residues: 1-574 <PAK>
A,Cross-references: GB:M31559
                                                                                                                                                                                                                                                                                       HRL 246
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Caccession: 167419
R;Chandrasekher, Y.A.; Melner, M.H.; Nagalla, S.R.; Stouffer, R.L.
Endocrinology 135, 307-314, 1994
A;Fitle: Progesterone receptor, but not estradiol receptor, messenger ribonucleic acid in A;Reference number: 153287; MUID:94283272; PMID:8013365
A;Accession: 167419
A;Accession: 167419
A;Accession: 167419
A;Accession: 167419
A;Accession: 167419
A;Accession: 167419
A;Cossereferences: UNIPROT:P49886; GB:S71040; NID:9547182; PIDN:AAB31102.1; PID:9547183
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: steroid hormone receptor; zinc finger
F;1-54/Domain: erba transforming protein homology (fragment) <ERBA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 LFAPNILLIDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFX 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 XXXXXXXXEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LSSTLKSLEBEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLILSHIRHMSNKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 44.5%; Score 547.5; DB 2; Length 121; Best Local Similarity 91.0%; Pred. No. 3.5e-47; Matches 11; Conservative 1; Mismatches 9; Indels 1;
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Search completed: November 8, 2004, 08:28:28 Job time : 12.049 secs

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(without alignments)
2338.928 Million cell updates/sec
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/cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pcp:
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  number of hits satisfying chosen parameters:
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                                                                                                           protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 8. Appli	Sequence 4. Appli	Sequence 8, Appli
DI	US-10-157-899A-2	US-10-157-899A-4	US-09-853-033-2	US-10-148-835-1	US-10-148-835-2	US-10-148-835-9	US-10-148-835-5	US-10-148-835-3	US-10-148-835-4	US-10-148-835-10	US-10-148-835-8	US-09-853-033-4	US-10-157-899A-8
80	14	14	6	14	14	14,	14	14	14	14	14	σ	14
* Query Match Length DB ID	414	438	595	595	595	595	595	595	595	595	595	099	414
Query Match	98.1	98.1	98.1	98.1	98.1	98.1	97.8	97.6	97.5	97.5	97.4	97.4	97.4
Score	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1202.5	1200.5	1199.5	1199.5	1198.5	1198.5	1197.5
Result No.	-	7	m	4	S.	9	7	80	6	10	11	12	13

14,	Sequence 19, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 17, Appl	2, Ar	Sequence 10, Appl	H	~	Sequence 9, Appli	7	14	61	128,	25,	6	Sequence 13, Appl	14	'n	7	ý	Sequence 7, Appli	42	73	69	71,	67,	10,	16,	8, Ap	-	Sequence 6, Appli
us-		14 US-10-052-092-10	14 US-10-437-107-10	14 US-10-278-481-17	9 US-09-933-267A-2	10 US-09-952-680A-10	13 US-10-096-710-1	13 US-10-081-563-2	14 US-10-052-092-9	14 US-10-052-092-13	14 US-10-052-092-14	14 US-10-207-655-61	14 US-10-177-293-128	14 US-10-157-899A-55	14 US-10-437-107-9	14 US-10-437-107-13	14 US-10-437-107-14	14 US-10-095-373A-2	14 US-10-392-274-2	14 US-10-148-835-6	L4 US-10-148-835-7	14 US-10-144-198-42	14 US-10-095-373A-73	14 US-10-095-373A-69	14 US-10-095-373A-71	14 US-10-095-373A-67	14 US-10-157-899A-10	L4 US-10-157-899A-16	9 US-09-853-033-8	L5 US-10-355-218-10	14 US-10-157-899A-6
438	211	547	547	591	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	595	676	677	726 1	727	414 ]	438 1	5 099	242	414 1
5 97.4	97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	5 97.4	97.4	5 97.4	5 97.4	5 97.4	5 97.3	5 97.3	5 97.2	5 97.1	97.0
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# ALIGNMENTS

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DEPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Kathryn Rene
APPLICANT: Ge los Angeles, Joseph Ernest
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kander, Gary Michael
APPLICANT: Serby, Dennis
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
CURRENT APPLICATION NUMBER: US/10/157,899A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/294,839
PRIOR APPLICATION NUMBER: US 60/294,839
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and a OTHER INFORMATION: zinc finger array(C7)
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96.3%; Pred. No. 2.2e-125;
cive 0; Mismatches 8;
Sequence 2, Application US/10157899A
Publication No. US20030143559A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.1
Best Local Similarity 96.3
Matches 237; Conservative
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TYPE: PRT
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61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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Publication No. US20030207380A1
GENERAL INFORMATION:
APPLICANT: SAITO et al.
TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
FILE REPERENCE: 2185-0648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SEQ ID NO 1
LENGTH: 595
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Sequence 2, Application US/09853033
| Sequence 2, Application US/09853033 |
| Patent No. US20020100068A1 |
| GENERAL INPORMATION: |
| APPLICANT: CHAMBON, PIERE |
| APPLICANT: CHAMBON, PIERE |
| TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION |
| TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER |
| FILE REFERENCE: 065691/0222 |
| CURRENT APPLICATION NUMBER: US/09/853,033 |
| CURRENT FILING DATE: 2000-10-65-11 |
| PRIOR PILING DATE: 2000-10-03 |
| SOFTWARE: PatentIN Ver: 2.1 |
| SSQ ID NO 2 |
| LENGTH: 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1206.5; DB 9; Length 595;
Pred. No. 3.5e-125;
0; Mismatches 8; Indels 1;
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Best Local Similarity 96.3%;
Matches 237; Conservative
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CORGANISM: Homo sapiens
US-09-853-033-2
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ORGANISM: Homo sapiens
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US-10-148-835-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Kathryn Rene
APPLICANT: Bracken, Michael
APPLICANT: Huang, Ying
APPLICANT: Huang, Ying
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kander, Gary Michael
APPLICANT: Zerby, Dennis
TITLE OF INVENTION: NOVEL ESTROGEN RECEPTOR LIGAND BINDING DOMAIN VARIANTS AND NOVEL
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
CURRENT APPLICATION NUMBER: US 60/294,839
PRIOR APPLICATION NUMBER: US 60/294,839
PRIOR PILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Fusion of the human-Estrogen-receptor-ligand-binding-domain and ; OTHER INFORMATION: zinc finger array(C7)
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              PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                         182 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
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ance 4, Application US/10157899A
F. Ication No. US20030143559A1
GENERAL INFORMATION:
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96.3%;
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ORGANISM: Artificial Sequence
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-148-835-9
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                                                  424
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                                                                                                                                                                                                     Sequence 2, Application US/10148835
ication No. US20030207380A1
RAL INFORMATION:
APPLICANT: SAITO et al.
TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
TITLE OF PELLE REFERENCE: 2185-0648P
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
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Publication No. US20030207380A1
GENERAL INFORMATION:
TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
FILE REPRENCE: 2.185-0648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT APPLICATION NUMBER: US/10/148,835
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 595
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96.3%; Pred. No. 3.5e-125;
tive 0; Mismatches 8;
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Best Local Similarity 96.3;
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                 LDAHRL 549
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US-10-148-835-2
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US-10-148-835-9
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Sequence 5, Application US/10148835

Publication No. US20030207380A1

GENERAL INFORMATION:

APPLICANT: SAITO et al.

TILLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

CURRENT APPLICATION NUMBER: US/10/148,835

CURRENT APPLICATION NUMBER: US/10/148,835

CURRENT APPLICATION NUMBER: US/10/148,835

CURRENT PILING DATE: 2002-10-11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO. 5

LENGTH: 595
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     Length 595;
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                                                  8; Indels
  DB 14;
Score 1206.5; DB 14
Pred. No. 3.5e-125;
0; Mismatches 8;
Query Match
Best Local Similarity 96.3%;
Matches 237; Conservative (
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US-10-148-835-5
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  425 FDMLLATSSRFRMANLQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
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Publication No. US20030207380A1
GENERAL INFORMATION:
APPLICANT: SAITO et al.
TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
FILE REFERENCE: 2185-0648P
CURRENT APPLICATION NUMBER: US/10/148,835
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
LENGTH: 595
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Sequence 8, Application US/10148835

Sequence 8, Application No. US20030207380A1

Sequence 10.220030207380A1

GENERAL INFORMATION:

APPLICANT: SAITO et al.

TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION

FILE REFERENCE: 2185-0648P

CURRENT APPLICATION NUMBER: US/10/148,835

CURRENT FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 213

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 595
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Matches 236, Conservative
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, ORGANISM: Homo sapiens

US-10-148-835-8
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ORGANISM: Homo sapiens
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US-10-148-835-3
; Sequence 3, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT PILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PALENTIN Ver. 2.0
; SEQ ID NO 3
; LENGTH: 595
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| Publication No. US20030207380A1
| GENERAL INFORMATION: | Applicant: SAITO et al. | Applicant: SAITO et al. | E OF INVENTION: | E REFERENCE: 2185-0648P
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Best Local Similarity 95.9%; Pred. No. 2.1e-124;
Matches 236; Conservative 0; Mismatches 9; Indels
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Pred. No. 1.7e-124;
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CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 213
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 595
TYPE: PRT
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95.9%;
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Whe hes 236; Conservative
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ORGANISM: Homo sapiens
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US-10-148-835-4
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Best Local &
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THER INFORMATION: Homosapiens-Bacteriophage P1
853-033-4
                                                                  1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                      Gaps
     DB 14; Length 595;
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TITLE OF INVENTION: TRANSGENIC MOUSE FOR TARGETED RECOMBINATION
TITLE OF INVENTION: MEDIATED BY MODIFIED CRE-ER
FILE REFERENCE: 065691/022
CURRENT APPLICATION NUMBER: US/09/853,033
CURRENT FILING DATE: 2001-05-11
PRIOR PRILICATION NUMBER: FR 00/12570
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 14
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                                    8; Indels
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97.4%; Score 1198.5; DB 1.
llarity 95.5%; Pred. No. 2.8e-124;
Conservative 2; Mismatches 8;
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Patent No. US20020100068A1;
GENERAL INFORMATION:
APPLICANT: CHAMBON, PIERRE
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ORGANISM: Artificial sequence
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Best Local Similarity 95.9
Matches 236; Conservative
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                 Similarity
                                   235;
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LENGTH: 660
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APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: Huang, Yilig
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kadan, Michael Joseph
APPLICANT: Seander, Gary Michael
APPLICANT: Earby, Dennis
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 4-32018A
CURRENT APPLICATION NUMBER: US 60/10/157, 899A
CURRENT PILLIG DATE: 2002-09-12
PRIOR PILLING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain
OTHER INFORMATION: and a zinc finger array(C7)
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APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: de los Angeles, Joseph Ernest
APPLICANT: Huang, Ying
APPLICANT: Kadan, Michael Joseph
APPLICANT: Kander, Gary Michael
APPLICANT: Estby, Dennis
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: LIGANDS AND PHARMACEUTICAL COMPOSITIONS
CURRENT REPERBURE: 4-32018A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/294,839
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Publication No. US20030143559Al
GENERAL INFORMATION:
Sequence 8, Application US/10157899A
Publication No. US20030143559A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Job time: 38,151 secs
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                                                                                                                                                             ) OTHER INFORMATION: Fusion of a mutated human-Estrogen-receptor-ligand-binding-domain; OTHER INFORMATION: and a zinc finger array(C7)
US-10-157-899A-14
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Publication No. US20030186385A1

GENERAL INFORMATION:

APPLICANT: Koide, Shohei

ITILE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND

TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF

FILE REPERENCE: 176/60901

CURRENT APPLICATION NUMBER: US/10/006,760

CURRENT APPLICATION NUMBER: 60/249,756

OR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PALENCHIN VOF: 2.1

SEQ ID NO 19

LENGTH: 511
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OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: lexA-ER(alpha)EF fusion protein
US-10-006-760-19
                                                                                                                                                                                                                                            Score 1197.5; DB 14;
Pred. No. 2.4e-124;
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Best Local Similarity 95.9%; Pred. No. 2.9e-124;
Matches 236; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                    1; Mismatches
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 438
                                                                                                                                                                                                                                            97.48;
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ORGANISM: Artificial Sequence
                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 95.5
Matches 235; Conservative
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LDAHRL 390
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US-10-006-760-19
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                                                                                                    TYPE: PRT
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Sequence 17, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appli
                                                              November 8, 2004, 08:16:47; Search time 14.5592 Seconds (without alignments) 1120.546 Million cell updates/sec
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                                                                                                                                       1 SLALSLTADQMVSALLDAEP......CKNVVPLYDLLLEMLDAHRL 246
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-980-115-12

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US-08-650-940-3

US-08-566-660-3

US-08-566-660-3

US-08-566-60-3

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US-08-836-620A-16

US-08-836-620A-10

US-08-836-620A-9

US-08-836-620A-9

US-08-836-620A-13

US-08-836-620A-13

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US-08-836-620A-13

US-08-836-620A-13

US-08-836-620A-13

US-08-836-620A-13

US-08-93-668-5

US-09-608-088-5

US-09-608-088-5

US-09-711-288-5

US-09-711-288-5

US-09-711-288-5

US-09-617-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            protein search, using sw model
                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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1230
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Maximum DB seq length: 2000000000
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                                            OM protein
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## ALIGNMENTS

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ORIGINAL SOURCE
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APPLICANT: Scanlan, Thomas S.
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Wagner, Richard L.
APPLICANT: Wagner, Richard L.
APPLICANT: Washner, Peter J.
APPLICANT: Washner, Parian L.
APPLICANT: Wash Andrew K.
ITILE OF INVENTION: NUCLEAR RECEPTOR LIGAND BINDING DOMAINS
FILE REPERBNCE: UCAL-246/0203
CURRENT APPLICATION NUMBER: US/08/980,115
CURRENT FILING DATE: 1996-12-13
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 595
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                                                                                                                                                                                                                        PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                                                                                            FDMLLATSSRFRMMNLOGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
                                                                                                                                                                                                                                                                                                               FDMLLATSSRFRMMILQGEEFVCLKSIIILINSGVYTF-LSSTLKSLEEKDHIHRVLDKIT 483
                                                                                                                                                                                                                                                                                                                                                           DTLIHLMAKAGLTLQQQHQRLAQLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
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                                                                                 Length 595;
                                                                                                                      Indels
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                                                                                     DB 3;
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Pred. No. 3.1e-134;
0; Mismatches 8;
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                                                                                     Score 1206.5; DB 3 Pred. No. 3.1e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (287)..(549)
; OTHER INFORMATION: minimal ligand binding domain US-08-980-115-12
                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08980115
Patent No. 6266622
GENERAL INFORMATION:
                                                                                   98.1%;
96.3%;
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Best Local Similarity 96.3%;
Matches 237; Conservative
                                                                                   Query Match 98.1
Best Local Similarity 96.3
Matches 237; Conservative
                          , MOLECULE TYPE: protein US-08-764-870-12
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LOCATION: (287)..
STRANDEDNESS:
TOPOLOGY: li
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305 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364
                                               PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                           FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
                                                                                                                                                                            FDMLLATSSRFRMMLQGEEFVCLKSI1LLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 960550.4
FILING DATE: 15-MAR-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
FRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
FILING DATE: 08-MAY-1996
FILING DATE: 08-MAY-1996
FILING DATE: 08-MAY-1996
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orphan receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/08836620A Patent No. 5958710 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
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Best Local Similarity 95.9
Matches 236; Conservative
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305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364
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                                                                                                       Sequence 2, Application US/08453998
Patent No. 6444438
GENERAL INFORMATION:
APPLICANT: METZGER, DANIEL
APPLICANT: MHTE, JOHN
TITLE OF INVENTION: BY YEASTS USING AN INDUCIBLE SYSTEM, VECTORS AND TITLE OF INVENTION: CORRESPONDING TRANSFORMED STRAINS
INUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,998
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/161,064
FILING DATE: 03-DE-1993
ATTORNEY/AGENT INFORMATION:
NAME: CLARAIN, MARLANA K.
REGISTRATION NUMBER: 35,843
REFERENCE/DOCKET NUMBER: 1037/98493
TELECOMMULCATION INFORMATION:
TELEPHONE: 220-861.3711
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Pred. No. 3.6e-133;
0; Mismatches 9;
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
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ilarity 95.9%;
Conservative
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: peptide
544 LDAHRL 549
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STRANDEDNESS: si
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Best Local Similarity
Matches 236; Conserv
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                                                                                        US-08-453-998-2
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              305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASWMGLLTNLADRELVHMINWAKRV 364
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                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Diego
STATE: California
COUNTRY: United States
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
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95.9%; Pred. No. 3.6e-133;
live 0; Mismatches 9;
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPONE: (619) 535-9001
TELEPAX: (619) 635-9001
                                                                                                                                                                                                                                                                     Sequence 35, Application US/09041886
Patent No. 6235872
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                                                                                                         241 LDAHRL 246
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Best Local Similarity
                                                                                                                                                    544 LDAHRL 549
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600 LDAHRL 605
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US-08-564-264-1
                                                                                                                               RESULT 7
US-09-566-660-3
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                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Yee, Jiing-Kuan
APPLICANT: Friedman, Theodore
APPLICANT: Friedman, Theodore
TITLE OF INVENTION: Useful in the Generation of Packaging Cell Lines for TITLE OF INVENTION: Pseudotyped Retroviral Vectors
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 SLALSLITADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 420
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95.9%; Pred. No. 4.1e-133;
iive 0; Mismatches 9;
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MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DISKETTE DOSTRAING SYSTEM: DOS SOFTWARE: FASISEO for Windows Version 2.0 CURRENT APPLICATION NUMBER: US/08/693,940 FILING DATE: PADGE CLASSIFICATION NUMBER: US/08/693,940 CLASSIFICATION NUMBER: BPIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNS/AGENT INFORMATION: NAME: Francis, Carol L REGISTRATION NUMBER: 36,513 REFERENCE/DOCKET NUMBER: 6510-055001 TELECOMMUNICATION INFORMATION: CEOSTRATION: MATERIAL CONTINUES CONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
                                                                                                                                                          Sequence 3, Application US/08693940 Patent No. 6133027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acids
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Matches 236; Conservative
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   544 LDAHRL 549
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ZIP: 9430
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CDECULE TYI;
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US-08-693-940-3
                                                                                             RESULT 6
US-08-693-940-3
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DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Multi-chimeric transactivating factor
US-09-566-660-3
                                                                    APPLICANT: Yee, Jiing-Kuan
APPLICANT: Yee, Jiing-Kuan
APPLICANT: Triedmann, Theodore
APPLICANT: Chen, Shin-Tai
TITLE OF INVENTION: Inducible Expression System
FILE REPERENCE: 6510-055CON
CURRENT APPLICATION NUMBER: US/09/566,660
CURRENT PILING DATE: 2000-05-08
PRIOR PILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 651
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
; Sequence 3, Application US/09566660; Patent No. 6432705
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APPLICANT: STEWART,
TITLE OF INVENTION: RECOMBINAT
TITLE OF INVENTION: RECOMBINAT
TITLE OF INVENTION: RECEPTOR:
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Nikaido, Marmels
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 DTLIHLMAKAGLTLQQQQQQQQLLLILLSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 358
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                                                                                                                                                   95.9%; Score 1180; DB 6; Length 410; 95.5%; Pred. No. 2.5e-131; tive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patepaten Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/836,620A
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Pred. No. 1.3e-129;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
; APPLICATION NUMBER: US/07/134,130
; FILING DATE: 17-DEC-1987
; PRIOR APPLICATION DATA:
; SEQ ID NO:5:
; LENGTH: 410
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APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08836620A
Patent No. 5958710
GENERAL INFORMATION:
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amino acid
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                                                                                                                                                                                             Conservative
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TITLE OF INVENTION:
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                                                                                                                                                                    Best Local Similarity
Matches 235; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYFF-LSSTLKSLEEKDHIHRVLDKIT 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    662 DTLIHLMAKAGLTLQQQQHQRLAQLLLISHIRHMSNKGMEHLYSMKCKUVVPLYDLLLEM 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60
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; PALCHAN: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLIAIS,
PIERRE; DEJEAN, ANNE
; TILLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED
; PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA
; UNMER OF SQUENCES: 11
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Pred. No. 5.2e-133;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (429-773)
OTHER INFORMATION: /note= "Estrogen binding domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "FLP recombinase domain."
                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "Linker peptide.
                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/02088
FILING DATE: 28-UTW-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 110 298.2
FILING DATE: 28-UTN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                          P564-5019
                                                              APPLICATION NUMBER: US/08/564,264
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         NAME: Murray, Robert B. REGISTRATION NUMBER: 22,980
                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
ORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.9%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature (1-423)
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(424-428)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (429-773)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
  OPERATING SYSTEM:
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LDAHRL 727
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                                                                                    FILING DATE
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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61 NQGKCVEGMVEIFDMLLATSSRFRMMLQGEEFVCLKSIILLNSGVYFF-LSSTLKSLEE 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 NQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 KDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 ELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 961.5; DB 2; Length 243;
Pred. No. 1e-105;
0; Mismatches 9; Indels 1:
                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Orphan receptor
NUMBER OF SEQUENCES: 19
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible bo
OPERATING SYSTEM: PC-DOS/MS-DS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,620A
FILING DATE:
                                                                                                                                                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-5EP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
                                             Orphan receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB 9609576.5
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Patent No. 5958710
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APPLICATION NUMBER: GB 960
FILING DATE: 08-MAY-1996
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.9%;
Matches 188; Conservative
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                     APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-836-620A-10
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APPLICANT: Cleaver, Brian
APPLICANT: Green, Mike L.
TITLE OF INVENTION: Materials and Methods for Detection and Quantitation of an Analy
FILE REPERENCE: ELI-101XC1
CURRENT APPLICATION NUMBER: US/09/660,979
CURRENT FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: 6/153,627
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.0
                                                                   310 SPALSLTADQWVSALLDAEPPLIYSEYDPSRPFSEASMMGLLTNLADRELVHMINWAKRV 369
                                                                                                                                                                                                                                                         DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240
                                                                                                                                   61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                                                                                                                370 PGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 429
                                                                                                                                                                                                                              FDMLLATSSRFRWMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEKDHIHRVLDKIT 180
                                                                                                                                                                                                                                                                                                                                                                  DTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGMEHLYNMKCKNVVPLYDLLLEM 548
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                                             1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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Gaps
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93.2%; Score 1146; DB 4; Length 264;
Best Local Similarity 91.5%; Pred. No. 1.4e-127;
Matches 225; Conservative 7; Mismatches 12: Indele
12; Indels
5; Mismatches
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10-08-886-620A-10
; Sequence 10, Application US/08836620A
; Patent No. 5958710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09660979; Patent No. 6500629; GENERAL INFORMATION:
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                LDAHRL 246
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549 LDAHRL 554
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TYPE: PRT
ORGANISM: Equus
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US-09-660-979-1
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INFORMATION FOR SEC ID NO:
                                                                                                                                                             Query Match
Best Local Similarity
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                                                        TYPE: amin
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 NQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXX 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQGKCVEGWVEIFDMLLATSSRFRMMILQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEE
                                                                                                                                                                                                                                                                                                                                                                                                   Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08836620A

Patent No. 5958710

Patent No. 5958710

Patent INFORMATION:

TITLE OF INVENTION: Orphan receptor

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,620A
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.4%; Score 951.5; DB 2; Best Local Similarity 93.4%; Pred. No. 1.5e-104; Matches 185; Conservative 2; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03933
FILING DATE: PELIOR DATE:
APPLICATION NUMBER: GB 9518272.1
FILING DATE: 08-SEP-1995
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9605550.4
FILING DATE: 15-MAR-1996
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9607532.0
FILING DATE: 11-APR-1996
APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
                                            PRIOR APPLICATION NOMBER: OB 92182/2.1
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: GB 960550.4
FILING DATE: 15-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION WINBER: GB 9607532.0
FILING DATE: 11-APR-1996
PRIOR APPLICATION NUMBER: GB 9609576.5
FILING DATE: 08-MAY-1996
INFORWATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGRATION AMINO acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
APPLICATION NUMBER: PCT/EP96/03933
                                   GB 9518272.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 95
APPLICATION NUMBER: GB 95
                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-08-836-620A-8
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                                                                                                                                                                                                                                                                                                                               49 ELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDR
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                                                                                                                                                                                                                          Query Match 77.0%; Score 946.5; DB 2; Length 243; Best Local Similarity 92.9%; Pred. No. 6e-104; Matches 184; Conservative 2; Mismatches 11; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 2, Application US/09893666A | Patent No. 6759568 | GENERAL INFORMATION: GFORMATION: GENERAL INFORMATION: FILE REFERENCE: 21021US-652-7249-0 | FILE REFERENCE: 21021US-652-7249-0 | CURRENT APPLICATION NUMBER: US/09/893,666A | PRIOR FILING DATE: 2002-02-12 | PRIOR PILING DATE: 2000-08-17 | NUMBER OF SEQ ID NOS: 7 | SOFTWARE: Patentin Version 3.1 | SEQ ID NO 2 | LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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64.4%; Score 792.5; DB 4
Best Local Similarity 63.0%; Pred. No. 3.9e-85;
Matches 155; Conservative 39; Mismatches 43
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8
                                                  LENGTH: 243 amino acids TYPE: amino acid
                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Rattus rattus
                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryzias latipes
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5.1.6 Compugen Ltd. GenCore version (c) 1993 - 2004 Copyright

OM protein - protein search, using sw model

8, 2004, 08:04:31; Search time 59.2408 Seconds (without alignments) 1489.639 Million cell updates/sec November Run on:

US-09-830-693B-28 1230 Title: Perfect score:

1 SLALSLTADQMVSALLDAEP......CKNVVPLYDLLLEMLDAHRL Sequence:

246

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 seqs, 358729299 residues ched:

number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_23Sep04:* Database

geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2001s:* geneseqn2003as:* geneseqn2003as:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aae35275 C7LBDAS f	Aab61498 Protein e	v		Aab36684 Mammalian	9	ß	6		Abb76378 Human nuc	Adp05661 Human nuc	Ado42788 Wild type	Ado42830 Human oes	Aab26784 Oestrogen	0	Aag84509 Human oes	ß	Aab26782 Oestrogen	Ado42820 Mutant hu	Abil5106 LBDG1 rel	Aag84507 Human oes	Ado42789 Mutant hu	Aag84508 Human oes	Aag84514 Human oes	Aag84512 Human oes
	OT .	AAE35275	AAB61498	AAE35276	AAB61499	AAB36684	AAY21626	AAG84505	AAG84513	AAG84506	ABB76378	ADP05661	ADO42788	AD042830	AAB26784	AAB26780	AAG84509	ADO42815	· AAB26782	ADO42820	ABJ15106	AAG84507	ADO42789	AAG84508	AAG84514	AAG84512
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	Score	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1206.5	1202.5	1202.5	1202.5	1202.5	1202	1201.5	1200.5	1200.5	1200.5			1198.5
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ABB76379 ABP70164 AAE35278	AAE33281 ADE39222 AAU98984 ADB99352	AAY33506 AAG84511 AAG84510 AAG68251	AAU98987 AAU98983 AAU98988 ABB09265	ABP70163 ABB81783 ABG76090 ABR47448 ABU09033
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24 24 28	330	ш ш ш ш 4 п й	16884 17860	44444 422

## ALIGNMENTS

AAE35275 standard; protein; 414 AA. RESULT 1 AAE3527! 

AAE35275;

(first entry) 28-MAY-2003

C7LBDAS fusion (wild-type) protein.

Oestrogen receptor; ER alpha; ligand binding domain; genetic disease; acquired disease; cell proliferative disorder; cancer; adenocarcinoma; LBD; gene switch; transgenic animal; transgenic; gene therapy; human; zinc finger array; C7; fusion protein.

Homo sapiens. Unidentified. Chimeric.

WO200297050-A2.

05-DEC-2002.

31-MAY-2002; 2002WO-US016946.

31-MAY-2001; 2001US-0294839P.

(NOVS ) NOVARTIS AG.

Kadan MJ, Huang Y, De Los Angeles JE, Bracken KR, Zerby DB;

Ksander GM;

WPI; 2003-156794/15. N-PSDB; AAD53875 New mutant estrogen receptor ligand binding domain capable of interacting with non-endogenous ligand, useful e.g. in combination with a ligand for constructing selective molecular gene switches for regulating gene

Example 4; Page 117-118; 159pp; English.

function.

The invention relates to a mutant osstrogen receptor (ER) alpha-ligand binding domain (LBD) which comprises an amino acid modification in region 1, region 2 or both and interacting with a non-endogenous ligand as a result of the amino acid modification. Sequences of the invention are useful for treatment of genetic diseases, acquired diseases and any other conditions including cell proliferative disorders such as cancer e.g.

are useful for the preparation of therapeutic agents for treating cancer, osteoporosis and other bone disorders, Alzheimer's disease and cardiovascular diseases

1,

Gaps

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Length

DB 4;

Score 1206.5; DB 4; Pred. No. 2.2e-134; 0; Mismatches 8;

98.1%; 96.3%;

Matches 237; Conservative

Н 132

> В ò g ò g ઠ 임 ò g

Similarity

Query Match Local

Sequence 422 AA;

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120

251

191

SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV

SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV

PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI

61 192

9

180

FDMLLATSSRFRWMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEKDHIHRVLDKIT

121 252

FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT

370

DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLYDLLEM

246 LDAHRL 376

LDAHRL

241

311

181

C7LBDBS fusion (wild-type) protein.

(first entry)

28-MAY-2003

AAE35276;

AAE35276 standard; protein; 438 AA

AAE35276 RESULT

DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM

240

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adenocarcinomas and other malignancies such as colon cancers, renal-cell carcinoma, prostate cancer, non-small cell carcinoma of the lung, cancer of the small intestine and cancer of the oesophagus. The invention is useful for constructing selective molecular gene switches for regulating gene function in plants and transgenic animals. It is also useful in gene therapy. The present sequence is human ER alpha LBD -zinc finer array (C7) fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; estrogen receptor alpha; cancer; osteoporosis; bone; Alzheimer's;
                                                                                                                                                                                                                      122 SLALSLTADOWVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                          PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
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breast, lymphoid, gastrointestinal, genito-urinary tract
                                                                                                                                           DB 6; Length 414;
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Pred. No. 2.1e-134;
0; Mismatches 8;
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illarity 96.3%;
Conservative
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                                                                                                                                                       Similarity
                                                                                                                  Sequence 414 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular
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New mutant estrogen receptor ligand binding domain capable of interacting with non-endogenous ligand, useful e.g. in combination with a ligand for constructing selective molecular gene switches for regulating gene
                                                                           Oestrogen receptor; ER alpha; ligand binding domain; genetic disease; acquired disease; cell proliferative disorder; cancer; adenocarcinoma; LBD; gene switch; transgenic animal; transgenic; gene therapy; human; zinc finger array; C7; fusion protein.
                                                                                                                                                                                                                                                                                                      Ksander
                                                                                                                                                                                                                                                                                                      Kadan MJ,
                                                                                                                                                                                                                                                                                                      Huang Y,
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                                                                                                                                                                                                                                                         31-MAY-2001; 2001US-0294839P.
                                                                                                                                                                                                                                  31-MAY-2002; 2002WO-US016946.
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                                                                                                                                                                                                                                                                                (NOVS ) NOVARTIS AG
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                                                                                                                                                                                     WO200297050-A2
                                                                                                                                       Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                                      Bracken KR,
Zerby DB;
                                                                                                                                                                                                            05-DEC-2002
                                                                                                                                                               Chimeric.
                                                                                                                                                                                                                                                                                                                    Zerby
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Novel isoforms of human estrogen receptor alpha useful for preparing therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease and cardiovascular diseases.

(EUMO-) EURO MOLECULAR BIOLOGY LAB

99IT-MI001433

29-JUN-1999;

27-JUN-2000; 2000WO-EP005981

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Denger S,

Gannon F,

WPI; 2001-137955/14.

The present invention relates to a human estrogen receptor (hER)-alpha isoform. Molecules which modulate the activity of the estrogen receptor

Claim 4; Page 45-46; 53pp; English

and cardiovascular diseases.

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1;
The invention relates to a mutant oestrogen receptor (ER) alpha-ligand binding domain (LBD) which comprises an amino acid modification in region 1, region 2 or both and interacting with a non-endogenous ligand as a result of the amino acid modification. Sequences of the invention are useful for treatment of genetic diseases, acquired diseases and any other conditions including cell proliferative disorders such as cancer e.g. lung, breast, lymphoid, gastrointestinal, genito-urinary tract adenocarcinomas and other malignancies such as colon cancers, renal-cell carcinoma, prostate cancer, non-emall cell carcinoma of the lung, cancer of the small intestine and cancer of the osophagus. The invention is useful for constructing selective molecular gene switches for regulating gene function in plants and transgenic animals. It is also useful in gene therapy. The present sequence is human ER alpha LBD -zinc finer array
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDMLLATSSRPRMMVLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEBKDHIHRVLDKIT 180
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                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                   Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by human estrogen receptor alpha isoform #2
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Pred. No. 2.3e-134;
0; Mismatches 8;
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96.3%;
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thes 237; Conservative
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Novel isoforms of human estrogen receptor alpha useful for preparing therapeutic agents for treating cancer, osteoporosis, Alzheimer's disease

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Flouriot

Denger S,

Gannon F,

WPI; 2001-137955/14.

(EUMO-) EURO MOLECULAR BIOLOGY

99IT-MI001433

29-JUN-1999;

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                                                  The present invention relates to a human estrogen receptor (hER)-alpha isoform. Molecules which modulate the activity of the estrogen receptor are useful for the preparation of therapeutic agents for treating cancer, osteoporosis and other bone disorders, Alzheimer's disease and cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel two hybrid detection method comprising fusing two proteins with a DNA binding sequence and a transcription activation sequence respectively for detecting interaction of the proteins in mammalian cells.
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                                                                                                                                                                                                                                                                                                                                    SLALSLTADÓMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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                                                                                                                                                                                                                                                                                                                        PDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT
                                                                                                                                                                                                                                                                                                                                                                             DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                                                                                                                                                                               SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                   PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalian; two-hybrid assay; hybrid protein; hybrid gene; detection; reporter gene; DNA-binding region; transcriptional activation; fused protein; protein interaction.
                                                                                                                                                                                     1;
                                                                                                                                                          DB 4; Length 457;
                                                                                                                                                                                   Indels
                                                                                                                                                         Score 1206.5; DB 4;
Pred. No. 2.4e-134;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalian two-hybrid protein SEQ ID NO:8.
                          Claim 4; Page 46-48; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB36684 standard; protein; 480 AA.
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                                                                                                                                                         98.1%;
96.3%;
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                                                                                                                                                     Query Match
Best Local Similarity 96.3
Matches 237; Conservative
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N-PSDB; AAC88199.
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                                                                                                                                 Sequence 457 AA;
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EXEXOCOCOXX
SXCCCCCCX
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WPI; 1999-357810/30
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                   The present invention describes a method for detecting the interaction of a first and a second protein within a mammalian cell. The method comprises a fusion protein of the first protein with two or more transcription activation sequences (which may be the same or different), and a fusion protein of the second protein with a DNA-binding sequence. These are expressed in a mammalian cell containing DNA carrying a reporter gene downstream of a sequence binding to the DNA-binding sequence, and the expression of the reporter gene is detected to indicate interaction of the two proteins. The method is useful for the mammalian cell, and screening of potential interactions within the mammalian cell, and screening of potential drugs targeting them. The present sequence represents a hybrid protein from an example given in the
                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                       174 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                              234 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSWEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                                                                                                                                                                                                                                                                                                          294 FDMLLATSSRFRMMULQGEEFVCLKSIILLNSGVYTF-LSSTLKSLEEKDHIHRVLDKIT
                                                                                                                                                                                                                                                                                                                                                                                          DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                                                                                                                                                                                                                                                                                                             FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT
                                                                                                                                                                                                                                                    SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                                                                                                                                                                                                                                                                                  PGFVDLTLHDQVHLLECAWLE1LM1GLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVE1
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                               1;
                                                                                                                                                                                                        DB 4; Length 480;
                                                                                                                                                                                                       Score 1206.5; DB 4; Length
Pred. No. 2.6e-134;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thyroid hormone replacement therapy; nuclear receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ligand binding domain of nuclear receptor hER
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Shiau AK;
 Example 2; Page 35-37; 63pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY21626 standard; protein; 595 AA.
                                                                                                                                                                                                        98.1%;
96.3%;
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West BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                      LDAHRL 246
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                                                                                                                                                                                                                  Local Similarity
es 237; Conser
                                                                                                                                                             present invention
                                                                                                                                                                                   Sequence 480 AA;
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Apriletti JW,
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                                                                                                                                                                                                                    hormone receptor that comprises administration of an aromatic compound which fits spatially and preferentially into a thyroid hormone ligand binding domain. The aromatic compound (of a specified formula) can be used to increase alpha-gleerophosphate dehydrogenase (GPDH) levels, at indicated in the treatment of obesity. The compound also lower total plasma cholesterol and triglyceride levels and can be used as anti-hypertriglyceridaemic agents. The compound may also be used for treating atheroselerosis and may be indicated in the indicated to the compound the present the compound the present of the compound the passes of the passes 
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                                                                                                                                                                                      The invention relates to a method for modulating activity of a thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DILIHLMAKAGLILQQQHQRLAQLILILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
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Pred. No. 3.5e-134;
0; Mismatches 8; Indels
Modulating activity of a thyroid hormone receptor
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                                                                                             Fig 3G-R; 447pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the nuclear receptor superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG84505 standard; protein; 595 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.1%;
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Best Local Similarity
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The present invention relates to ligand dependent transcriptional factors including oestrogen receptor (ER) alpha and beta protein, glucocorticoid receptor protein (GR), minerablocorticoid receptor protein (RR), progesterone protein (PR), progesterone receptor protein (PR), progesterone receptor protein (PR), progesterone receptor protein (PR), thyroid hormone receptor protein (PR), the mucleic acids encoding them and cells comprising them and a specified reporter gene for the ligand dependent transcriptional factor. These proteins are useful in the modulation of ligand dependent transcriptional factor activity. The cells, mutant ERalpha and the polymucleotide encoding it may be used in assays for qualitatively analysing an activity for transactivation of a reporter gene by a test ERalpha, for screening mutant ligand dependent transcriptional factors, for evaluating an activity for transactivation of a reporter gene by a test ERalpha and/or for screening activity for transactivation of a reporter gene by a test ERalpha and/or for screening activity for transactivation of a reporter gene by a test ERalpha and/or for screening a compound useful for treating a disorder of a mutant
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                                       glucocorticoid receptor protein; GR; mineralocorticoid receptor protein; MR; peroxisome proliferator-activated receptor protein; PPAR; Progesterone receptor protein; PR; pregname X receptor protein; PXR; thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR; transactivation; ERalpha; breast cancer; mutant; mutein.
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                           dependent transcriptional factor; oestrogen receptor; ER;
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21-JUL-2000; 2000JP-00220508.
02-AUG-2000; 2000JP-00234053.
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99JP-00370667
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                                                                                                                                                                   Homo sapiens
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27-DEC-1999;
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Cativity. The cells, mutant ERalpha and the polynucleotide encoding it may be used in assays for qualitatively analysing an activity for transcriptional factors, for everening cativity for transcriptional factors, for evaluating and/or companied acceptor process for screening activity for transcriptional factors, for evaluating and/or for for evaluating and compound useful for treating a disorder of a mutant
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0; Mismatches 8;
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                                   21-JUL-2000; 2000JP-00220508.
02-MG-2000; 2000JP-00234653.
03-AUG-2000; 2000JP-00235460.
03-AUG-2000; 2000JP-00235461.
03-AUG-2000; 2000JP-00235461.
                                                                                                                                                               (SUMO ) SUMITOMO CHEM CO LID
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nes 237; Conservative
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Gaps

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Score 1206.5; DB 4; Length 595; Pred. No. 3.5e-134; 0; Mismatches 8; Indels 1;

120 424 180

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RESULT 9 AAG84506

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SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
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    98.1%;
96.3%;
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Ligand dependent transcriptional factor; oestrogen receptor; ER; glucocorticoid receptor protein; GR; mineralocorticoid receptor protein; R; peroxisome proliferator-activated receptor protein; PPAR; progesterone receptor protein; PR; pregname X receptor protein; PXR; thyroid hormone receptor protein; TR; vitamin D receptor protein; VDR; transactivation; ERalpha; breast cancer; mutant; mutein.
                                                                                                                                                                                                                                                                                                                       Human oestrogen receptor alpha protein mutant K303R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 170-174; 276pp; English.
                                                                                                                                                                                                      AAG84506 standard; protein; 595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-DEC-1999; 99JP-00348022.
27-DEC-1999; 99JP-0037667.
07-JUL-2000; 2000JP-00207011.
21-JUL-2000; 2000JP-00226508.
02-AUG-2000; 2000JP-00234053.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saito K, Ohe N, Satoh H;
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-367866/38.
                                                             LDAHRL 246
                                                                                                      544 LDAHRL 549
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                                                             241
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                          484
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A transgenic mouse, useful in screening for medicaments for the treatment of e.g., diabetes or skin cancers, comprises a fusion protein between a recombinase Cre, and a modified ligand binding domain of the nuclear
Oestrogen; receptor; human; transgenic mouse; cytostatic;
antiinflammatory; antidiabetic; endocrine; anorectic; hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is the protein sequence of the human nuclear oestrogen receptor alpha (1). The invention relates to a non-human
                                                                                                                                                                                                                                                                                                                                                                                                         'note= "ligand-binding domain"
                                                                                                                                                                                                                               180. .262
'note= "DNA-binding domain"
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                                                                                                                                                                                                                                                                         263. .301
/note= "D hinge region"
302. .552
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                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2001; 2001WO-IB002246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2000; 2000FR-00012570.
11-MAY-2001; 2001US-00853033.
```

Sequence 595 AA;

metazoan organism, especially a transgenic mouse, characterised in that
at least one cell comprises: (i) a fusion protein formed from a
cecombinase (Creb, a hinge region (preferably human (I) b hinge), and a
modified ligand binding domain (IBD) of a nuclear osetrogen receptor,
especially human (I), its fragment or variant; and (ii) one or more genes
cor DNA sequences of interest belonging to the genome of the organism,
into which one or more recognition sites of the recombinase protein are
the second inserved. The (I) LBD domain is preferably modified by a 6321R, 6400V, or
cecombinase activity in the presence of a natural ligand such as
coestradiol, but recombinase activity is induced by a small quantity of a
synthetic ligand that has antioestrogenic activity, e.g. tamoxifen or 4bydroxytamoxifen. The metazoan organism or its cells, such as epidermal
cells, hepatcoytes or adipocytes, are useful in carrying out a
spatiotemporally controlled site-specific recombination of a DNA sequence
of interest in its natural chromatin environment. It is also used in
creening of medicaments for pathological conditions associated with an
alteration of the expression and/or function of the DNA sequence of
interest, such as skin cancer, inflammation, diabetes, alopecia, obesity, or in promoting hepatic regeneration 

Sequence 595 AA;

PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180 DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240 1 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 60 1; DB 5; Length 595; 8; Indels 98.1%; Score 1206.5; DB 5, 96.3%; Pred. No. 3.5e-134; 0; Mismatches Best Local Similarity 96.3 Matches 237; Conservative LDAHRL 246 LDAHRL 549 61 365 Query Match 121 425 181 484 241 544 g 요 g g ሯ 용 ઠે δ 8

(first entry) 26-AUG-2004 ADP05661;

ADP05661 standard; protein; 595 AA

Human nuclear receptor protein SeqID35

disease risk, disorder risk; mutation; polymorphism; muclear receptor protein; antibacterial; antithyroid; cardiovascular-Gen; cytostatic; dermatological; eating-Disorders-Gen; gastrointestinal-Gen; gynaecological; hepatotropic; immunosuppressive; muscular-Gen; nephrotropic; osteopathic; virucide; adrenal gland; colon; cardiovascular; intestine; kidney; liver; lung; muscular; ovary; blood; prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus; pancreas; bone; joint; breast; immune system; metabolic; nutritive disease; human.

Homo sapiens

WO2004045369-A2

03-JUN-2004

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This invention relates to a novel method of determining whether a patient has an increased risk for developing a disease or disorder which comprises determining the presence of a mutation or polymorphism in the patient of patient's gene encoding a nuclear receptor protein or measuring the expression or level of biological activity of a nuclear receptor copypositide in the patient or in a cell of the patient. The invention may be useful for the development of compounds with an antibacterial, antithyroid, cardiovascular-Gen, cytostatic, dermatological, eatingantithyroid, cardiovascular-Gen, cytostatic, dermatological, eatingantithyroid, agartointestinal-Gen, gynaecological, hepatotropic, immunosuppressive, muscular-Gen, nephrotropic, osteopath; or virucide activity. The method is useful for determining whether a patient has an increased risk for developing a disease or disorder. The nucleic acid concoding a nuclear receptor polypeptide, an expression vector comprising the nucleic acid operably linked to a promoter, or a compound that condulates the biological activity of a nuclear receptor polypeptide, is useful for treating or preventing a disease or disorder of the adrenal gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular, ovary, blood, prostate, skin, spleen, stomach, testes, thymus, thyroid, uterus, pancreas, bone and joints, breast, or immune system, or metabolic or nutritive disease or disorder. The present sequence is that of a nuclear receptor protein which may be used in the method of the
                                                                                                                                                                                                                                                                                                            Determining an increased risk for e.g. colon, brain or breast disease or disorder, by detecting a mutation or polymorphism in the nuclear receptor gene, or measuring expression or biological activity level of the nuclear
                                                                                                                                                                     Li F;
Zeng H;
                                                                                                                                                                     JE, Gracerov A, Hohmann J,
Pavlova MN, Vassilatis D,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 35; 508pp; English.
                      12-NOV-2003; 2003WO-US036229.
                                                                    14-NOV-2002; 2002US-0426305P.
                                                                                                                                                                     Bergmann JE,
                                                                                                                                                                                            Mcilwain KL,
                                                                                                                                                                                                                                          WPI; 2004-449627/42.
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                                                                                                                     (NURA-) NURA INC
                                                                                                                                                                     Gaitanaris GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
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Sequence 595 AA;

120 305 SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV 364 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYFF-LSSTLKSLEEKDHIHRVLDKIT 483 DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 240 9 484 DTLIHLMAKAGLTLQQQQQQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI Gape 1; 98.1%; Score 1206.5; DB 8; Length 595; 96.3%; Pred. No. 3.5e-134; ive 0; Mismatches 8; Indels 1; Query Match 98.1 Best Local Similarity 96.3 Matches 237; Conservative LDAHRL 246 549 LDAHRL 121 61 365 425 181 241 544

음 8 유 ò 셤 ò 유 ò RESULT 12 AD042788 ΩI

AD042788 standard; protein; 595 AA.

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New mutant estrogen receptor-alpha useful for determining effectiveness of treatment by estrogen receptor activity regulator substance and
                                                                           receptor-alpha; ER; ER activity regulator substance;
                                             protein
                                             Human oestrogen receptor-alpha (ER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 19; 111pp; Japanese.
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15-NOV-2002; 2002JP-00331995.
15-NOV-2002; 2002JP-00331996.
                                                                                                                                                                                                                    14-NOV-2003; 2003WO-JP014494.
                                                                                                                                                                                                                                                                                                                (SUMO ) SUMITOMO CHEM CO LTD.
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              (first entry)
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nes 237; Conservative
                                                                                           anti-oestrogen substance
                                                                                                                                                                                                                                                                                                                                                                                                                                        antiestrogen substance
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                                                                                                                                                        WO2004046352-A1.
                                                                                                                          Homo sapiens
              26-AUG-2004
                                                                                                                                                                                       03-JUN-2004
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                                                                                                        human; oestrogen receptor-alpha; ER; ER activity regulator substance; anti-oestrogen substance.
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Pred. No. 3.5e-134;
0; Mismatches 8; Indels 1;
                                                                           Wild type human oestrogen receptor-alpha (ER) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1; 111pp; Japanese.
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15-NOV-2002; 2002JP-00331995.
5-NOV-2002; 2002JP-00331996.
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                                             (first entry)
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Best Local Similarity 96.3
Matches 237; Conservative
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              AD042788
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The invention comprises the amino acid sequences of mutant human oestrogen receptor-alpha (ER) proteins. The mutant ER proteins of the invention are useful for determining the effectiveness of a treatment by an ER activity regulator substance, and for determining the effectiveness of a treatment by an anti-oestrogen substance. The present amino acid sequence represents a human ER protein.
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                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                     DB 8; Length 595;
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                  98.1%; Score 1206.5; DB 8; 96.3%; Pred. No. 3.5e-134; ive 0; Mismatches 8;
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ADO42830

RESULT 13
ADO42830
ID ADO42
XX
AC ADO42

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hypertension; diabetes; obesity; glaucoma; depression; wound;
protein co-ordinate data; thyroid hormone receptor; oestrogen receptor.
               Homology model; ligand binding domain; glucocorticoid receptor; AIDS;
     Destrogen receptor protein sequence.
                                                                            99GB-00004441.
                                                                   01-MAR-2000; 2000WO-GB000727
                                                                                                      dillner M, Greenidge P;
                                                                                            (KARO-) KARO BIO AB.
                                              40200052050-A2.
                                   Unidentified.
                                                                            01-MAR-1999;
                                                                                  22-APR-1999;
                                                        08-SEP-2000.
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WPI; 2000-549565/50.

Designing a homology model of the ligand binding domain of a glucocorticoid receptor displayed as a three-dimensional image, useful for identifying agonists and antagonists for treating e.g. inflammation, hypertension, glaucoma, diabetes.

Disclosure; Fig 6; 246pp; English.

This invention relates to a method for designing an homology model of the ligand binding domain of a glucocorticoid receptor. The homology model cay be displayed as a three-dimensional image. The method comprises: (a) providing an amino acid sequence and an x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domain of the glucocorticoid receptor and the thyroid, oestrogen or progesterone receptor; (b) modifying the accuracy of the homology, cor progesterone receptor; (c) verifying the accuracy of the homology, model by comparing it with experimentally-determined binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying the homology model for greater consistency with the binding properties. The homology model is useful for drug screening and designing ligands (agonists and antagonists) capable of binding to a glucocorticoid receptor. The identified agonists are useful for the treatment of phenical phenical infammation and also in immunosuppressive therapy. The identified but and also in immunosuppressive therapy and detains the homology models are also useful for electronic screening of compound databases, de novo drug design and/or prediction of binding and wounds. The homology models are also useful for electronic screening of compound databases, de novo drug design and/or prediction of binding contains enthality and phenical phenical phenical processions. The specification contains protein contains and and and arrangement and and arrangement and and experience and contains and contains and arrangement and and arrangement and and arrangement and oestrogen and progesterone receptors. The present sequence represents an oestrogen receptor protein. The protein is used in an example of the method of the invention for homology modelling of a glucocorticoid receptor based on the thyroid and oestrogen receptors.

Sequence 244 AA;

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61 PGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI 120
                                                                        9
                                                                                                         9
                                                                                         PGFVDLTLHDQVHLLECAWLE1LMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEI
                                                                      SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV
                                      Gaps
                                      1;
   DB 3; Length 244;
97.8%; Score 1202.5; DB 3; Length 96.3%; Pred. No. 3e-134; ive 0; Mismatches 8; Indels
Query Match
Best Local Similarity 96.3
Matches 236; Conservative
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240
FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFXXXXXXXXXEEKDHIHRVLDKIT 180
                   DTLIHLMAKAGLTLQQQQQQQQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM 239
   DTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEM
                                                      AAB26780 standard; protein; 244 AA.
                             245
                                    244
                             LDAHR
                                    LDAHR
                                                              AAB26780;
121
              181
                     180
                             241
                                               RESULT 15
                                                   AAB26780
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Homology model; ligand binding domain; glucocorticoid receptor; AIDS; hypertension; diabetes; obesity; glaucoma; depression; wound; human; protein co-ordinate data; thyroid hormone receptor; oestrogen receptor. WO200052050-A2. Homo sapiens

Human oestrogen receptor protein sequence.

18-JAN-2001 (first entry)

08-SEP-2000

01-MAR-2000; 2000WO-GB000727

99GB-00004441. 99GB-00009151. 01-MAR-1999; 22-APR-1999;

(KARO-) KARO BIO AB.

Greenidge Gillner M,

WPI; 2000-549565/50.

Designing a homology model of the ligand binding domain of a glucocorticoid receptor displayed as a three-dimensional image, useful for identifying agonists and antagonists for treating e.g. inflammation, hypertension, glaucoma, diabetes.

Disclosure; Fig 2A; 246pp; English.

This invention relates to a method for designing an homology model to ligand binding domain of a glucocorticoid receptor. The homology model may be displayed as a three-dimensional image. The method comprises: (a) providing an amino acid sequence and an x-ray crystallographic structure of the ligand binding domain of a thyroid, oestrogen or progesterone ceceptor; (b) modifying the x-ray crystallographic structure to take account of differences between the amino acid configuration of the ligand binding domain of the glucocorticoid receptor and the thyroid, oestrogen, binding domain of the glucocorticoid receptor and the thyroid, oestrogen, cr progesterone receptor; (c) verifying the accuracy of the homology model for preater consistency with the binding properties of a number of ligands for the glucocorticoid receptor; and (d) modifying the homology model for greater consistency with the binding properties of a number of ligands for the glucocorticoid receptor. The identified agonists are useful for the treatment of inflammation and also in immunosuppressive therapy. The identified antagonists are useful for the treatment of antagonists are useful for the treatment of cobesity, glaucoma, depression, acquired immune deficiency syndrome (ADDS) and wounds. The homology models are also useful for electronic greening and wounds. The homology models are also useful for electronic screening of compound databases, de novo drug design and/or prediction of binding affinities of glucocorticoid receptor ligands for the receptor by

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molecular mechanics scoring functions. The specification contains protein co-ordinate data for the glucocorticoid receptor models produced using the method, based on the X-ray crystallographic structure of the cestrogen and progesterone receptors. The present sequence represents the human oestrogen receptor protein. The protein is used in an example of the method of the invention for homology modelling based on the thyroid
      888888888888
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Sequence 244 AA;

9 1 SLALSLTADOMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRV Gaps 1; Score 1202.5; DB 3; Length 244; Preq. No. 3e-134; 0; Mismatches 8; Indels 1; Query Match
Best Local Similarity 96.3%;
Matches 236; Conservative ò g

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PDMLLATSSRFRMANLOGEEFVCLKSIILLNSGVYFXXXXXXXXEEKDHIHRVLDKIT 180 121

121 FDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVTF-LSSTLKSLEEKDHIHRVLDKIT 179

LDAHR 245 241

Search completed: November 8, 2004, 08:26:23 Job time : 59.2408 secs

LDAHR 244

240